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(54) Title: COMPOSITIONS FROM THE GRASSES *LOLIUM PERENNE* AND *FESTUCA ARUNDINACEA*(57) Abstract: Isolated polynucleotides encoding polypeptides from *Lolium perenne* and *Festuca arundinacea* active in lignin, fructan and tannin biosynthetic pathways are provided, together with expression vector and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

Compositions from the grasses *Lolium perenne* and *Festuca arundinacea*.

COMPOSITIONS ISOLATED FROM FORAGE GRASSES
AND METHODS FOR THEIR USE

Reference to Related Applications

This application claims priority to U.S. Provisional Patent Application No. 60/337,703 filed November 7, 2001.

Technical Field of the Invention

This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the lignin, tannin and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

Background of the Invention

Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists

to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

Lignin Biosynthetic Pathway

5 Lignin is an insoluble polymer that serves as a matrix around the polysaccharide components of some plant cell walls, and that is primarily responsible for the rigidity of plant stems. Generally, the higher the lignin content, the more rigid the plant. For example, tree species synthesize large quantities of lignin, with lignin constituting 20%-30% of the dry weight of wood. The lignin content of grasses ranges from 2-8% of dry weight and changes
10 during the growing season. In addition to providing rigidity, lignin aids in water transport within plants by rendering cell walls hydrophobic and water impermeable. Lignin also plays a role in disease resistance of plants by impeding the penetration and propagation of pathogenic agents.

 Forage digestibility is affected by both lignin composition and concentration. Lignin
15 is largely responsible for the digestibility, or lack thereof, of forage crops, with small increases in plant lignin content resulting in relatively high decreases (> 10%) in digestibility (Buxton and Russell, *Crop. Sci.* 28:5358-558, 1988). For example, crops with reduced lignin content provide more efficient forage for cattle, with the yield of milk and meat being higher relative to the amount of forage crop consumed. During normal plant growth, an increase in
20 the maturity of the plant stem is accompanied by a corresponding increase in lignin content and composition that causes a decrease in digestibility. This change in lignin composition is to one of increasing syringyl:guaiacyl (S:G) ratio. When deciding on the optimum time to harvest forage crops, farmers must therefore choose between a high yield of less digestible material and a lower yield of more digestible material.

25 Lignin is formed by polymerization of three different monolignols, *para*-coumaryl alcohol, coniferyl alcohol and sinapyl alcohol, that are synthesized in a multistep pathway, with each step in the pathway being catalyzed by a different enzyme. The three monolignols are derived from phenylalanine or tyrosine in a multistep process and are then polymerized into lignin by a free radical mechanism. Following polymerization, *para*-coumaryl alcohol,
30 coniferyl alcohol and sinapyl alcohol are converted into the *p*-hydroxyphenyl (H), guaiacyl (G) and syringyl (S) units of lignin, respectively. While these three types of lignin subunits

are well known, it is likely that slightly different variants of these subunits may be involved in the lignin biosynthetic pathway in various plants. For example, studies suggest that both free monolignols and monolignol-4-coumarate esters may be substrates for lignin formation in grasses. The relative concentration of the monolignol residues in lignin varies among different plant species and within species. For example, the monolignol content for H/G/S of grasses, alfalfa and softwood gymnosperms is 22%/44%/34%, 7%/39%/54% and 14%/80%/6%, respectively (van Soest in "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY). The composition of lignin may also vary among different tissues within a specific plant.

Coniferyl alcohol, *para*-coumaryl alcohol and sinapyl alcohol are synthesized by similar pathways (Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998; Guo *et al.*, *Plant Cell* 13:73-88, 2001). The first step in the lignin biosynthetic pathway is the deamination of phenylalanine or tyrosine by phenylalanine ammonia-lyase (PAL) or tyrosine ammonia-lyase (TAL), respectively. In maize, the PAL enzyme also has TAL activity (Rosler *et al.*, *Plant Physiol.* 113:175-179, 1997). The product of TAL activity on tyrosine is 4-coumarate, whereas the product of PAL activity on phenylalanine is cinnamate which is then hydroxylated by cinnamate 4-hydroxylase (C4H) to form 4-coumarate. 4-Coumarate is hydroxylated by coumarate 3-hydroxylase (C3H) to give caffeate. The newly added hydroxyl group is then methylated by caffeic acid O-methyl transferase (COMT) to give ferulate. Several other methylation reactions can be catalyzed by COMT, including caffeoylaldehyde to coniferaldehyde, and 5-hydroxyconiferaldehyde to sinapaldehyde. 4-Coumarate, caffeate and ferulate can all be conjugated to coenzyme A by 4-coumarate:CoA ligase (4CL) to form 4-coumaryl CoA, caffeoyl CoA and feruloyl CoA, respectively. Caffeoyl CoA can then be methylated by the enzyme caffeoyl-CoA O-methyl transferase (CAMT).

Coniferaldehyde is hydroxylated to 5-hydroxyconiferaldehyde by ferulate 5-hydroxylase (F5H). Reduction of 4-coumaryl CoA, caffeoyl CoA and feruloyl-CoA to 4-coumaraldehyde, caffeoyl aldehyde and coniferaldehyde, respectively, is catalyzed by cinnamoyl-CoA reductase (CCR). Coumaraldehyde, caffeoyl aldehyde, coniferaldehyde and 5-hydroxyconiferaldehyde are further reduced by the action of cinnamyl alcohol dehydrogenase (CAD) to give coniferyl alcohol which is then converted into its glucosylated

form for export from the cytoplasm to the cell wall by coniferol glucosyl transferase (CGT). Recently a sinapyl alcohol dehydrogenase (SAD) was described that converts sinapaldehyde to sinapyl alcohol (Li *et al.*, *Plant Cell* 13:1567-1586, 2001). Following export, the de-glucosylated form of coniferyl alcohol is obtained by the action of coniferin *beta*-glucosidase (CBG). Finally, polymerization of the three monolignols to provide lignin is catalyzed by phenolase (PNL), laccase (LAC) and peroxidase (PER). For a more detailed review of the lignin biosynthetic pathway, see Whetton R and Sederoff R, *The Plant Cell*, 7:1001-1013, 1995 and Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998.

Both lignin levels and composition have been changed in a range of plant species by altering the expression of specific lignin biosynthetic enzymes. For example, anti-sense 4CL constructs in transgenic aspen trees reduced lignin content from 20 to 11% (a 45% reduction) but at the same time increased both cellulose levels (by 15%) and growth rate (Hu *et al.* *Nature Biotechnol.* 17:808-812, 1999). These trees had the same level of total carbon, suggesting that carbon partitioning had been altered. Reducing 4CL by either anti-sense or sense-suppression in tobacco plants led to an accumulation of hydroxycinnamic acids in cell walls as well as a reduction in both guaiacyl and syringyl lignin units (Kajita *et al.*, *Plant Cell. Physiol.* 37:957-965, 1996). In transgenic tobacco plants in which levels of C4H were reduced by anti-sense or sense suppression, total lignin content was reduced, in addition to a reduction in syringyl lignin units (Sewalt *et al.*, *Plant Physiol.* 115:41-50, 1997). Reducing the levels of PAL in tobacco plants by anti-sense or sense-suppression reduced total lignin content but did not change the syringyl-guaiacyl (S:G) lignin ration. In alfalfa, reducing expression of COMT through either anti-sense or gene silencing decreased total lignin by decreasing the amount of guaiacyl units and resulted in a near total loss of syringyl lignin units (Guo *et al.*, *Plant Cell* 13:73-88, 2001). In contrast, reducing CCOMT expression through anti-sense or gene silencing in alfalfa plants also decreased total lignin by reducing the total amount of guaiacyl lignin units but had no effect on the amount of syringyl lignin. Reducing CCR expression by anti-sense in tobacco plants resulted in reduced lignin content and increased S:G ratios due to lower guaiacyl lignin units (Piquemal *et al.*, *Plant J.* 13:71-83, 1998). *A. thaliana* plants where the F5H gene had been mutated contained only traces of syringyl lignin (Marita *et al.*, *Proc. Natl. Acad. Sci. USA* 96:12323-12332, 1999).

Alteration of grass lignin composition may usefully be employed to maintain high forage digestibility throughout the year. This is most important when the plant is approaching flowering and/or during flowering. At this time, the entire lignin biosynthetic pathway will preferably be reduced, in particular lowering the amount of syringyl lignin units, thereby lowering the S:G ratio and maintaining the digestibility of the forage crop.

Several of the enzymes involved in the lignin biosynthetic pathway also have other functions within the plant. For example, PAL is a key enzyme of plant and fungi phenylpropanoid metabolism and catalyzes the first step in phenylpropanoid metabolism. It is involved in the biosynthesis of a wide variety of secondary metabolites such as flavonoids, furanocoumarin in phytoalexins and cell wall components. These compounds have many important roles in plants during normal growth and in responses to environmental stress. PAL catalyzes the removal of an ammonia group from phenylalanine to form trans-cinnamate. PAL and the related histidine ammonia lyase are unique enzymes which are known to have the modified amino acid dehydroalanine (DHA) in their active site (Taylor *et al.*, *J. Biol. Chem.* 265:18192-18199, 1990). Phenylalanine and histidine ammonia-lyases (PAL) active site has a consensus of GTITASGDLVPLSYIA. The serine residue is central to the active site, and the region around this active site residue is well conserved (Langer *et al.*, *Biochem.* 33:6462-6467, 1994).

C4H, which is a member of the cytochrome P450 monooxygenase superfamily, plays a central role in both phenylpropanoid metabolism and lignin biosynthesis where it anchors a phenylpropanoid enzyme complex to the endoplasmic reticulum (ER). The phenylpropanoid pathway controls the synthesis of lignin, flower pigments, signaling molecules, and a large spectrum of compounds involved in plant defense against pathogens and UV light. This is also a branch point between general phenylpropanoid metabolism and pathways leading to various specific end products. 4CLs are a group of enzymes necessary for maintaining a continuous metabolic flux for the biosynthesis of plant phenylpropanoids, such as lignin and flavonoids that are essential to the survival of plants, because they serve important functions in plant growth and adaptation to environmental perturbations. Three isoforms of 4CL have been identified with distinct substrate preference and specificities. Expression studies in angiosperms revealed a differential behavior of the three genes in various plant organs and upon external stimuli such as wounding and UV irradiation or upon challenge with fungi.

One isoform is likely to participate in the biosynthetic pathway leading to flavonoids whereas the other two are probably involved in lignin formation and in the production of additional phenolic compounds other than flavonoids (Ehlting *et al.*, *Plant J.* 19:9-20, 1999).

5 F5H is involved in the phenylpropanoid biosynthesis pathway. It belongs to the CYP84 subfamily of the cytochrome P450 family and is known as cytochrome P450 84A1. F5H is one of the enzymes in the pathways leading to the synthesis of sinapic acid esters, but also has coniferaldehyde hydroxylase activity (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000). In the generalized pathway for phenylpropanoid metabolism, F5H catalyzes the formation of 5-hydroxyferulate (a precursor of sinapate) and sinapate in turn as the precursor
10 for sinapine and for sinapoyl CoA in two bifurcated pathways (Chapple *et al.*, *Plant Cell* 4:1413-1424, 1992). Sinapoyl CoA has been considered as the precursor for sinapyl alcohol, which is then polymerized into syringyl (S) lignin. In addition, CYP84 F5H product carries out the hydroxylation of coniferaldehyde (ConAld) to 5-OH ConAld (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000).

15 Peroxidases are heme-containing enzymes that use hydrogen peroxide as the electron acceptor to catalyze a number of oxidative reactions. They belong to a superfamily consisting of 3 major classes. Class III consists of the secretory plant peroxidases, which have multiple tissue-specific functions in removal of hydrogen peroxide from chloroplasts and cytosol, oxidation of toxic compounds, biosynthesis of the cell wall, defense responses towards
20 wounding, indole-3-acetic acid (IAA) catabolism and ethylene biosynthesis.

Fructan Biosynthetic Pathway

Plant carbohydrates can be divided into two groups depending on their function within the plant. Structural carbohydrates, such as cellulose, are usually part of the
25 extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-
30 359, 1999). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble

carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases urea production in animals as less protein is degraded in the rumen (Biggs and Hancock, *Trends in Plant Sci.* 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants, with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et*

al., (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnol.* 16:843-846; Hellwege *et al.*, *Proc. Nat. Acad. Sci. USA* 97:8699-8704, 2000).

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression (for a review see Smeekens, *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then dephosphorylated by SPP to form sucrose (Lunn *et al.*, *Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al.*, *Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at

least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and Campbell, *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. It hydrolyzes terminal non-reducing beta-D-fructofuranoside residues in beta-D-fructo-furanosides.

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

Tannin Biosynthetic Pathway

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock, resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive

value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

5 Much of the biosynthetic pathway for condensed tannins is shared with that for anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

10 Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to
15 naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- β -hydroxylase (F3 β H) to give dihydrokaempferol. The enzyme flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). The enzyme dihydroflavonol-4-reductase (DFR)
20 catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to galocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and
25 Morris P. in *Metabolic Engineering of Plant Secondary Metabolism*, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000.

30 While polynucleotides encoding some of the enzymes involved in the lignin, fructan and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been identified.

Thus there remains a need in the art for materials useful in the modification of lignin, fructan and tannin content and composition in plants, and for methods for their use.

Summary of the Invention

5 The present invention provides enzymes involved in the lignin, fructan or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base,
10 pseudostems, floral stems, roots, inflorescences and stems. The present invention also provides genetic constructs, expression vectors and host cells comprising the inventive polynucleotides, and methods for using the inventive polynucleotides and genetic constructs to modulate the biosynthesis of lignins, fructans and tannins.

 In specific embodiments, the isolated polynucleotides of the present invention
15 comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-62 and 125-162; (b) complements of SEQ ID NO: 1-62 and 125-162; (c) reverse complements of SEQ ID NO: 1-62 and 125-162; (d) reverse sequences of SEQ ID NO: 1-62 and 125-162; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%,
20 80%, 90% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("x-mers") of any of SEQ ID NO: 1-62 and 125-162; and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-62 and 125-162 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

25 In further aspects, the present invention provides isolated polypeptides comprising an amino acid sequence of SEQ ID NO: 63-124 and 163-190, together with polypeptides comprising a sequence having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 63-124 and 163-190. The present
30 invention also contemplates isolated polypeptides comprising at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a)

SEQ ID NO: 63-124 and 163-190; and (b) sequences having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, in combination with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopal synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

In yet another aspect, methods for modulating the lignin, fructan or tannin content and composition of a target organism, such as a plant, are provided, such methods including stably incorporating into the genome of the target plant a genetic construct comprising a polynucleotide of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. In a related aspect, a method for producing a plant having altered lignin, fructan or tannin

composition is provided, the method comprising transforming a plant cell with a genetic construct comprising of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

Brief Description of the Drawings

Fig. 1 shows the activity of recombinant LpSPP (SEQ ID NO: 8) and FaSPP (SEQ ID NO 7) on dephosphorylating Suc-6-P and Fru-6-P. The pET41a extract was the vector control.

Fig. 2 shows the peroxidase activity of PER3 (SEQ ID NO: 50) and PER5 (SEQ ID NO: 52) as determined by oxidation of ABTS. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control.

Fig. 3 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp6-SFT1 (SEQ ID NO: 3). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp6-SFT fragment was amplified using specific PCR primers.

Fig. 4 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp1-SST (SEQ ID NO: 1). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp1-SST fragment was amplified using specific PCR primers.

Plant number 5 is a non-transgenic control.

Fig. 5 shows the fructan level in transgenic *N. benthamiana* lines transformed with Lp6-SFT1 (SEQ ID NO: 3) and Lp1-SST (SEQ ID NO: 1).

Fig. 6 shows the sucrose synthesizing activity of FaSPS-N (SEQ ID NO: 9) with and without SPP (SEQ ID NO: 8) in mammalian cell extracts. The non-transfected cells are controls.

Fig. 7 shows the sucrose cleaving activity of FaSUS1 (SEQ ID NO: 13) in mammalian cell extracts.

Fig. 8 shows the invertase activity for vacuolar invertase (SEQ ID NO: 25) and two cell wall invertases (SEQ ID NO: 17 and 19); absence of invertase activity from an empty
5 vector (pPICZalphaA) control is also shown.

Detailed Description of the Invention

The polypeptides of the present invention, and the polynucleotides encoding the polypeptides, have activity in lignin, fructan and tannin biosynthetic pathways in plants.
10 Using the methods and materials of the present invention, the lignin, fructan and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the polynucleotides or polypeptides encoded by polynucleotides. The isolated polynucleotides and polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with
15 temperate pastures and to increase the yield of animal products from pastures.

The lignin, fructan and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding enzymes involved in the lignin, fructan or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified lignin, fructan and/or tannin content can be obtained by
20 transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the lignin, fructan and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of lignins, fructans or tannins having altered composition.

25 The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species, and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for
30 producing a plant having an altered genotype or phenotype is provided, such methods

comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-62 and 125-162 and their variants, may be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NO: 1-62 and 125-162, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 63-124 and 163-190. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in lignin, fructan and tannin biosynthetic processes:

TABLE 1

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
1 and 125	63 and 163	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from <i>Festuca arundinacea</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
2	64	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from <i>Festuca arundinacea</i> . It contains a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
3 and 126	65 and 164	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Festuca arundinacea</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 90 to 564). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
4 and 127	66 and 165	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Lolium perenne</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 96 to 107). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
5	67	Fructan biosynthesis	Homolog of sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Festuca arundinacea</i> .
6 and 128	68 and 166	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Lolium perenne</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			residues 90 to 103). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
7 and 129	69	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phosphohydrolase (SPP; EC 3.1.3.24) isolated from <i>Festuca arundinacea</i> . This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, <i>Trends Biochem Sci.</i> 23:127-129, 1998). Motif I (amino acid residues 10 to 19) contains conserved Asp and a Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
8	70	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phosphohydrolase (SPP; EC 3.1.3.24) isolated from <i>Lolium perenne</i> . This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, <i>Trends Biochem Sci.</i> 23:127-129, 1998). Motif I (residues 10 to 19) contains conserved Asp and Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (amino acid residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
9 and 130	71	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from <i>Festuca arundinacea</i> .
10 and 131	72 and 167	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from <i>Lolium perenne</i> and that is involved in the sucrose synthesis pathway.
11 and 132	73 and 168	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-N) isolated from <i>Lolium perenne</i> and that is involved in the sucrose synthesis pathway.
12 and 133	74 and 169	Fructan	Homolog of sucrose synthase (SuS) isolated

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	from <i>Lolium perenne</i> . These molecules contain a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz <i>et al.</i> , <i>Science</i> 240:1759-1764, 1988).
13	75	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Festuca arundinacea</i> . This molecule contains a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz <i>et al.</i> , <i>Science</i> 240:1759-1764, 1988).
14 and 134	76 and 170	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Lolium perenne</i> .
15	77	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Festuca arundinacea</i> .
16 and 135	78 and 171	Fructan biosynthesis	Homologue of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved peptide domain in amino acid residues 139 to 144 and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D (LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
17	79	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 70 to 74 and a peptide domain in amino acid residues 250 to 255. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 61 to 74 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
18 and 136	80 and 172	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases.
19	81	Fructan	Homolog of cell wall invertase (CWINV)

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 60 to 64. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 51 to 64 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 24.
20 and 137	82 and 173	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 61 to 66 and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
21	83	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 73 to 77 and a peptide domain in amino acid residues 253 to 258. The consensus peptide domain of invertases is (WVYL)EC(PIL)D-(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 64 to 77 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
22 and 138	84 and 174	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 174 to 179 and 234 to 239,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			respectively. The consensus peptide domain of invertases is (WVYL)EC- (PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
23	85	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 56 to 60. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 47 to 60 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 22.
24 and 139	86 and 175	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 244 to 249. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). They also contain a glycosyl hydrolases family 32 signature region at amino acid 56 to 69 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 25.
25 and 140	87 and 176	Fructan biosynthesis	Homolog of vacuolar invertase (SINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 136 to 140 and 138 to 142, respectively and a peptide domain in amino acid residues 317 to 322 and 319 to 324, respectively. The consensus peptide domain of

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 127 to 140 and 129 to 142 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
26 and 141	88 and 177	Fructan biosynthesis	Homolog of invertase (SINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 143 to 148 and 184 to 189, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
27	89	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium perenne</i> . The molecule has two conserved AMP binding regions at amino acid residues 182 to 193 and 383 to 389 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
28 and 142	90	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium perenne</i> . The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> ,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			<i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
29	91	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Festuca arundinacea</i> . The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
30 and 143	92 and 178	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium</i> . The molecules have two conserved AMP binding regions at amino acid residues 194 to 205 and 394 to 400 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
31	93	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Festuca</i>

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			<i>arundinacea</i> . The molecule has two conserved AMP binding regions at amino acid residues 194 to 206 and 482 to 490 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
32 and 144	94 and 179	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from <i>Lolium perenne</i> . The molecules have a conserved cytochrome P450 region in amino acids 436 to 445 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000).
33	95	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from <i>Festuca arundinacea</i> . The molecule has a conserved Cytochrome P450 region in amino acids 440 to 449 that contains a conserved Cys residue involved in heme binding. The cytochrome P450 cysteine heme-iron ligand signature consensus is FGxGRRSCPG where the conserved C is the heme iron ligand (Miles <i>et al.</i> , <i>Biochim. Biophys. Acta</i> 1543:383-407, 2000). It also contains an aldehyde dehydrogenases active site (Hempel <i>et al.</i> , <i>Adv. Exp. Med. Biol.</i> 436:53-59, 1999) at amino acid residues 428 to 435. A hydrophobic signal peptide region is present in amino acid residues 1 to 24.
34 and 145	96 and 180	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from <i>Lolium perenne</i> . These molecules contain a conserved zinc-containing alcohol dehydrogenase domain (Joernvall <i>et al.</i> , <i>Eur. J. Biochem.</i> 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. They also

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			contain a cytochrome C family heme-binding site signature (Mathews, <i>Prog. Biophys. Mol. Biol.</i> 45:1-56, 1985) in residues 45 to 50.
35	97	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from <i>Festuca arundinacea</i> . CAD belongs to the family of zinc-binding dehydrogenases. This molecule contains a conserved zinc-containing alcohol dehydrogenases domain (Joernvall <i>et al.</i> , <i>Eur. J. Biochem.</i> 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. It also contains a Cytochrome C family heme-binding site signature. The cytochrome C family heme-binding site signature is CGICHT. In the cytochrome C protein family, the heme group is covalently attached by thioether bonds to two conserved cysteine residues. The consensus sequence for this site is Cys-X-X-Cys-His and the histidine residue is one of the two axial ligands of the heme iron. This arrangement is shared by all proteins known to belong to cytochrome C family (Mathews, <i>Prog. Biophys. Mol. Biol.</i> 45:1-56, 1985).
36 and 146	98	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from <i>Lolium perenne</i> .
37	99	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from <i>Festuca arundinacea</i> .
38 and 147	100 and 181	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from <i>Lolium perenne</i> that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first specific step in the synthesis of the lignin monomers. A hydrophobic region typical of a signal peptide is present in amino acid residues 1 to 24.
39 and 148	101	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from <i>Festuca arundinacea</i> that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			specific step in the synthesis of the lignin monomers.
40 and 149	102 and 182	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Festuca arundinacea</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
41 and 150	103	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Lolium perenne</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
42	104	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Festuca arundinacea</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
43	105	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Lolium perenne</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
44 and 151	106 and 183	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from <i>Lolium perenne</i> . The molecules

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			have a conserved cytochrome P450 region in amino acids 463 to 472 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
45	107	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from <i>Festuca arundinacea</i> . The molecule has a conserved cytochrome P450 region in amino acids 462 to 471 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
46 and 152	108	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from <i>Lolium perenne</i> . The polypeptide has a conserved PAL-histidase region in amino acid residues 193 to 209.
47 and 153	109 and 184	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from <i>Festuca arundinacea</i> . A conserved phenylalanine and histidine ammonia-lyases active site signature has been identified in amino acid residues 195 to 210.
48	110	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved peroxidase I region is present in amino acid residues 188 to 199 and contains a conserved His residue at position 196 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 60 to 71, with a conserved His residue at position 69 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 27.
49	111	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 208 in the active site. A signal peptide is present in amino acid residues 1 to 33.
50	112	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 180 to 190 and contains a conserved His residue at position 188 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 66, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
51 and 154	113	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 207 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 70 to 80, with a conserved His residue at position 78 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 20.
52 and 155	114	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 198 to 208 and contains a conserved His residue at position 206 in the active site (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 34.
53, 156, and 162	115, 185, and 190	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 157 to 168, 188 to 199, and 190 to 201, respectively and contain a conserved His residue at position 165, 196 and 198, respectively in the active site, and the conserved peroxidase 2 region is present in amino acid residues 29 to 41, 60 to 72 and 62 to 74, respectively, with a conserved His residue at position 38, 69 and 71, respectively that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988).
54	116	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 176 to 186 and contains a conserved His residue at position 184 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 67, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
55	117	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI) isolated from <i>Lolium perenne</i> . The molecule contains a chalcone isomerase region at amino acid residues 1 to 213.
56	118	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI). The molecule contains a chalcone isomerase region at amino acid residues 23 to 235.
57 and 157	119 and 186	Tannin Biosynthesis	Homolog of Chalcone Synthase (CHS) isolated from <i>Lolium perenne</i> and that is an important enzyme in flavonoid synthesis. The molecules contain a conserved chalcone synthase active site (Lanz <i>et al.</i> , <i>J. Biol. Chem.</i> 266:9971-9976, 1991) at amino acid residues 166 to 175, with the conserved Cys residue at position 167.
58 and 158	120 and 187	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Festuca arundinacea</i> .
59 and 159	121 and 188	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Lolium perenne</i> .
60 and 160	122 and 189	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Lolium perenne</i> . These molecules contain a conserved ATP/GTP binding site at amino acid residues 84 to 91 and 86 to 93, respectively, known as the "A" sequence (Walker <i>et al.</i> , <i>EMBO J.</i> 1:945-951, 1982) or "P-loop" (Saraste <i>et al.</i> , <i>Trends Biochem. Sci.</i> 15:430-434, 1990).
61 and 161	123	Tannin biosynthesis	Homolog of flavanone 3- β hydroxylase (F3 β H) isolated from <i>Lolium perenne</i> .
62	124	Tannin Biosynthesis	Homolog of flavanone 3- β hydroxylase (F3 β H) isolated from <i>Festuca arundinacea</i> .

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

5 The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including RNAi, HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. A polynucleotide of the present invention
10 may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the
15 art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising variants of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising extended sequences
20 of SEQ ID NO: 1-62 and 125-162 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-62 and 125-162 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-62 and 125-162 (x-mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-62 and 125-162, all of
25 which are referred to herein, collectively, as "polynucleotides of the present invention." Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement(s)," "reverse complement(s)," and "reverse
30 sequence(s)," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

Preferably, sequences that are complements of a specifically recited polynucleotide
 5 sequence are complementary over the entire length of the specific polynucleotide sequence.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. The value of x may be from about 20 to about 600, depending upon the specific sequence.

10 Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-62 and 125-162, or their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 63-124
 15 and 163-190. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID
 20 NO: 1-62 and 125-162, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 63-124 and 163-190, or a variant
 25 thereof.

Polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries comprising forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide.
 30 Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial

sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (*x*-mer) of one of the sequences of SEQ ID NOS: 1-62 and 125-162 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-62 and 125-162.

The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides and functional portions of polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full length sequences corresponding to the sequences set out as SEQ ID NOS: 1-62 and 125-162. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NOS: 1-62 and 125-162 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for

example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The “sticky” ends ensure proper ligation when the two portions are hybridized. In this way, a
5 complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-62 and 125-162, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An
10 oligonucleotide probe or primer is described as “corresponding to” a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant of one of the specified sequences.

15 Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a
20 second DNA strand under stringent hybridization conditions.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to
25 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in
30 Dieffenbach and Dyksler, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for

designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

5 The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 were isolated from cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID
10 NOS: 1-62 and 125-162.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on
15 known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are
20 linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial isolated polynucleotide sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 63-124 and 163-190, as well as variants of such sequences.

25 As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence of the present invention encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been
30 transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and

higher eukaryotic cells. Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or 293T. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 63-124 and 163-190, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may

be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

5 As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably
10 at least 90%, more preferably yet at least 95% and most preferably, at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

15 Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-190 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide or polypeptide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with
20 a polynucleotide of the present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or
25 functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO;; or (2) they contain identifiable domains in common. Similarly, polypeptides having a specified degree of identity to a polypeptide of the present invention preferably additionally have at least one of the following features: (1) they have substantially the same functional properties as the polypeptide in the recited SEQ ID NO;; or (2) they contain identifiable domains in common.

30 Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another

polynucleotide or polypeptide, using computer algorithms that are publicly available. The BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11 [Jan-20-2000] and Version 2.2.1 [Apr-13-2001] set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of

polypeptide sequences: blastall -p blastp -d swissprot -e 10 -G 0 -E 0 -v 30 -b 30 -i queryseq -o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The percentage identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion

of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the
5 BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each
10 of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set
15 at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a
20 variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to
25 a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C.
30 Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as

probe composition, presence of organic solvents, and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes
5 each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide
10 of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse sequences, or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide
15 sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 63-124 and 163-190 as a result of amino acid substitutions,
20 insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a lignin, fructan or tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a
25 functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For applications where amplification of lignin, fructan or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number
30 of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of lignin, fructan or tannin synthesis is desired, the open reading frame may be

inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting
5 appropriate sequences or subsequences (*e.g.*, DNA or RNA) in ribozyme constructs.

Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are
10 not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'- non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of lignin, fructan or tannin synthesized by the plant by the process of
15 cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally
20 positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrsen, *Mol. Gen. Genet.* 225:81-93, 1991). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic
25 constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic constructs of the present invention are well known in the art. The promoter gene sequence,
30 and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the

promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter, will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer

resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, in Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988).

5 Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic
10 construct of the present invention may be linked to a vector having at least one replication system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of
15 plants, both monocotyledonous (*e.g.*, grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the
20 group consisting of *Lolium perenne* and *Festuca arundinacea*. Other plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* (hybrid ryegrass), *Lolium rigidum* (Wimmera grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above,
25 transformation of a plant with a genetic construct of the present invention will produce a modified lignin, fructan or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be
30 transformed with more than one construct of the present invention, thereby modulating the lignin, fructan and/or tannin biosynthetic pathways by affecting the activity of more than one

enzyme, affecting enzyme activity in more than one tissue or affecting enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme.

- 5 The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a lignin, fructan or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

- 10 Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous
- 15 plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be
- 20 usefully employed in the inventive methods include those taught by Ellis *et al.*, *Plant Cell Reports*, 8:16-20, 1989; Wilson *et al.*, *Plant Cell Reports* 7:704-707, 1989; Tautorius *et al.*, *Theor. Appl. Genet.* 78:531-536, 1988; Hiei *et al.*, *Plant J.* 6:271-282, 1994; and Ishida *et al.*, *Nature Biotechnol.* 14:745-750, 1996; US Patent 5,591,616; and European Patent Publication EP 672 752 A1. Once the cells are transformed, cells having the inventive DNA construct
- 25 incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is
- 30 employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced

sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. For a review of techniques of gene suppression see *Science*, 288:1370-1372, 2000. Exemplary gene silencing methods are also provided in WO 99/49029 and WO 99/53050. Posttranscriptional gene silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have provided evidence that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, e.g., review by Montgomery and Fire, *Trends in Genetics*, 14: 255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene silencing. A unique feature of this posttranscriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene-silencing effects may be disseminated to other parts of an organism and even transmitted through the germ line to several generations.

The polynucleotides of the present invention may be employed to generate gene silencing constructs and or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript and sense and antisense sequences, as well as splice junction sequences, bind together to form double-stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases bind to and cleave the double-stranded RNA, thereby initiating the cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are

delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (e.g., in high-throughput screening of sequences), and
5 studying their functions in intact organisms.

Example 1

ISOLATION OF CDNA SEQUENCES FROM *L. PERENNE* AND *F. ARUNDINACEA* CDNA LIBRARIES

10 *L. perenne* and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected include those obtained from leaf blades, leaf base, pseudostem, floral stems, inflorescences, roots and stem. Total
15 RNA was isolated from each tissue type using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP
20 using a ZAP Express cDNA Synthesis Kit (Stratagene, La Jolla, CA), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene, La Jolla, CA) employing 1 µl of sample DNA from the 5 µl ligation mix. Mass excision of the libraries was done using XL1-Blue MRF' cells and XL0LR cells (Stratagene, La Jolla, CA) with ExAssist helper phage (Stratagene, La Jolla,
25 CA). The excized phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG). Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was
30 purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a

Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 4, 6, 11, 127, 128 and 132 were identified from *L. perenne* leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 1, 14, 15, 26, 32, 36, 38, 41, 49, 125, 134, 141, 144, 147, and 150 were identified from *L. perenne* vegetative stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 17, 22, 25, 138, and 140 were identified from *L. perenne* leaf and pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 43, 57, 61, 157, and 161 were identified from *L. perenne* pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 10, 12, 28, 30, 34, 44, 60, 131, 133, 142, 143, 145, 151, and 160 were identified from *L. perenne* floral stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 8, 18, 46, 52, 53, 55, 59, 136, 152, 155, 156, 159, and 162 were identified from *L. perenne* stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 51 and 154 were identified from a *L. perenne* root cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 24, 27 and 139 were identified from *L. perenne* leaf blade cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 9, 37, 39, 40, 45, 130, 148, and 149 were identified from *F. arundinacea* basal leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 19, 21, 29, 33, 35, 47, 48, and 153 were identified from *F. arundinacea* combined day 3 and day 6 basal leaves cDNA expression libraries; the polynucleotide sequence identified as SEQ ID NO: 54 was identified from a *F. arundinacea* combined day 3 and day 6 leaves cDNA expression library; the polynucleotide sequence identified as SEQ ID NO: 56 was identified from a *F. arundinacea* inflorescence cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 20 and 137 were identified from a subtracted *F. arundinacea* leaf blade cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 7, 23, 42, 50, 62, and 129 were identified from *F. arundinacea* pseudostem cDNA expression libraries; the polynucleotide

sequences identified as SEQ ID NO: 2, 13, 16 and 135 were identified from *F. arundinacea* leaf cDNA expression libraries; and the polynucleotide sequences identified as SEQ ID NO: 3, 5, 31, and 126 were identified from a *F. arundinacea* inflorescence day 0 cDNA expression library.

5

BLASTN Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the EMBL DNA database were made as of October 19, 2001 using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastn -d embldb -e 10 -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o. Comparisons of DNA sequences provided in SEQ ID NOS: 125-162 to sequences in the EMBL DNA database were made using BLASTN algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastn -d embldb -F F -e 10 -G0 -E0 -r 1 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NO: 4-6, 9-11, 17-19, 21-26, 33, 44, 45, 48, 49, 51-55, 59, 60, 130-132, 136, 139, 146, 151, 154-156, 159, and 162 were determined to have less than 50% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 2, 3, 7, 8, 14, 16, 36-38, 46, 47, 50, 56-58, 61, 129, 135, 137, 138, 152, 153, 157, 158, 160 and 161 were determined to have less than 75% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 1, 12, 13, 15, 20, 28, 31, 32, 35, 40 62, 125-128, 133, 134, 142, 144 and 147 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequences of SEQ ID NOS: 29, 30, 39, 41-43, 141, 143, 148, and 149 were determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

BLASTP Polypeptide Analysis

The protein sequences corresponding to the isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm

BLASTP. Comparisons of protein sequences provided in SEQ ID NOS: 63-124 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastp -dstdb-e 10 -G0 -E0 -v 30 -b 30 -i queryseq -o. Comparisons of protein sequences provided in SEQ ID NOS: 163-190 to sequences in the SwissProt/Trembl protein database were made using BLASTP algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastp -d stdb -F F -e 10 -G0 -E0 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NOS: 65-68, 72, 73, 78, 80, 81, 84, 85, 87, 88, 106, 107, 110, 111, 113-115, 117, 118 and 121 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 71, 79, 82, 83, 86, 95, 98-100, 112, 116, 120, 122-124, 167, 168, 171-174, 185, 188, and 190 were determined to have less than 75% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 63, 64, 69, 70, 74-77, 90, 91, 93, 94, 97, 101, 102, 104, 108, 109, 119, 175, 183, 187, and 189 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NOS: 89, 92, 96, 103, 105, 163-165, 169, 170, 177, 179, 181, 184, and 186 were determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above.

BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTX algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastx -dstdb -e 10 -G0 -E0 -v 30 -b 30 -i queryseq -o. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made using BLASTX algorithm

Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastx -d stdb -F F -e 10 -G0 -E0 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NOS: 11, 44, 45, 48, 49, 51, 52, 55, 130, 132, 155, 156, and 162 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 3-10, 16-26, 33, 36-38, 40-43, 50, 53, 54, 56, 58-62, 129, 131, 135-139, 146, 150, 151, 154, and 158-161 were determined to have less than 75% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 1, 2, 12-15, 27, 28-32, 34, 35, 39, 46, 47, 57, 125-128, 133, 134, 141-145, 147-149, 152, 153, and 157 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. Finally, the sequence of SEQ ID NO: 140 was determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above.

The location of open reading frames (ORFs), by nucleotide position, contained within the sequences of SEQ ID NO: 1-62 and 125-162, and the corresponding amino acid sequences are provided in Table 2 below. SEQ ID NO: 1-8, 10-15, 17, 19, 21, 23-25, 28-52, 54-59, 61-62 and 125-162 are believed to contain full-length ORFs.

TABLE 2

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
1	56-2,020	63
2	64-2,010	64
3	64-1,926	65
4	74-1,945	66
5	40-1,911	67
6	79-1,938	68
7	246-1,514	69
8	264-1,532	70
9	84-3,272	71
10	73-3,297	72
11	129-2,942	73
12	46-2,472	74
13	113-2,539	75
14	61-2,505	76

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
15	103-2,253	77
16	3-1,439	78
17	26-1,777	79
18	2-1,174	80
19	59-1,852	81
20	2-1,201	82
21	1-1,779	83
22	198-1,097	84
23	27-1,772	85
24	36-1,802	86
25	78-2,084	87
26	2-1,423	88
27	3-1,622	89
28	85-1,764	90
29	72-1,751	91
30	127-1,800	92
31	137-1,810	93
32	62-1,567	94
33	80-1,597	95
34	32-1,117	96
35	86-1,171	97
36	55-852	98
37	75-872	99
38	149-1,240	100
39	90-1,118	101
40	28-1,110	102
41	66-1,148	103
42	64-1,146	104
43	85-1,170	105
44	88-1,683	106
45	93-1,721	107
46	111-2,246	108
47	144-2,285	109
48	22-993	110
49	4-1,038	111
50	87-1,067	112
51	59-1,135	113
52	18-1,052	114
53	1-882	115
54	80-1,015	116
55	322-1,014	117
56	172-762	118
57	118-1,299	119

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
58	5-595	120
59	14-1,003	121
60	1-987	122
61	65-1,174	123
62	103-1,245	124
125	55-2,019	163
126	63-1,925	164
127	73-1,944	165
128	71-1,930	166
131	72-3,299	167
132	134-2,950	168
133	45-2,471	169
134	65-2,512	170
135	74-1,819	171
136	170-1,855	172
137	28-1,770	173
138	26-1,733	174
139	35-1,801	175
140	71-2,083	176
141	63-1,607	177
143	126-1,799	178
144	61-1,566	179
145	67-1,152	180
147	148-1,239	181
149	27-1,109	182
151	87-1,718	183
153	143-2,284	184
156	46-1,017	185
157	117-1,313	186
158	81-1,193	187
159	12-1,001	188
160	26-1,018	189
162	50-1,027	190

SEQ ID NO: 125 and 163 are related to SEQ ID NO: 1 and 63, respectively; SEQ ID NO: 126 and 164 are related to SEQ ID NO: 3 and 65, respectively; SEQ ID NO: 127 and 165 are related to SEQ ID NO: 4 and 66, respectively; SEQ ID NO: 128 and 166 are related to SEQ ID NO: 6 and 68, respectively; SEQ ID NO: 129 is an extended sequence of SEQ ID NO: 7; SEQ ID NO: 130 is an extended sequence of SEQ ID NO: 9; SEQ ID NO: 131 and 167 are related to SEQ ID NO: 10 and 72, respectively; SEQ ID NO: 132 and 168 are related

to SEQ ID NO: 11 and 73, respectively; SEQ ID NO: 133 and 169 are related to SEQ ID NO: 12 and 74, respectively; SEQ ID NO: 134 and 170 are related to SEQ ID NO: 14 and 76, respectively; SEQ ID NO: 135 and 171 are full-length sequences of SEQ ID NO: 16 and 78, respectively; SEQ ID NO: 136 and 172 are full-length sequences of SEQ ID NO: 18 and 80, respectively; SEQ ID NO: 137 and 173 are related to SEQ ID NO: 20 and 82, respectively; SEQ ID NO: 138 and 174 are full-length sequences of SEQ ID NO: 22 and 84, respectively; SEQ ID NO: 139 and 175 are related to SEQ ID NO: 24 and 86, respectively; SEQ ID NO: 140 and 176 are related to SEQ ID NO: 25 and 87, respectively; SEQ ID NO: 141 and 177 are full-length sequences of SEQ ID NO: 26 and 88, respectively; SEQ ID NO: 142 is related to SEQ ID NO: 28 and encodes the same amino acid sequence; SEQ ID NO: 143 and 178 are related to SEQ ID NO: 30 and 92, respectively; SEQ ID NO: 144 and 179 are related to SEQ ID NO: 32 and 94, respectively; SEQ ID NO: 145 and 180 are full-length sequences of SEQ ID NO: 34 and 96, respectively; SEQ ID NO: 146 is related to SEQ ID NO: 36 and encodes the same amino acid sequence; SEQ ID NO: 147 and 181 are related to SEQ ID NO: 38 and 100, respectively; SEQ ID NO: 148 is related to SEQ ID NO: 39, and encodes the same amino acid sequence; SEQ ID NO: 149 and 182 are related to SEQ ID NO: 40 and 102, respectively; SEQ ID NO: 150 is related to SEQ ID NO: 41 and encodes the same amino acid sequence; SEQ ID NO: 151 and 183 is related to SEQ ID NO: 44 and 106, respectively; SEQ ID NO: 152 is related to SEQ ID NO: 46, and encodes the same amino acid sequence; SEQ ID NO: 153 and 184 are related to SEQ ID NO: 47 and 109, respectively; SEQ ID NO: 154 is related to SEQ ID NO: 51, and encodes the same amino acid sequence; SEQ ID NO: 155 is related to SEQ ID NO: 52, and encodes the same amino acid sequence; SEQ ID NO: 156 and 185 are full-length sequences of SEQ ID NO: 53 and 115, respectively; SEQ ID NO: 162 and 190 are variants of SEQ ID NO: 156 and 185, respectively, with a difference in the 5' region of SEQ ID NO: 156 and 162; SEQ NO: 157 and 186 are related to SEQ ID NO: 57 and 119, respectively; SEQ ID NO: 158 and 187 are related to SEQ ID NO: 58 and 120, respectively; SEQ ID NO: 159 and 188 are full-length sequences of SEQ ID NO: 59 and 121, respectively; SEQ ID NO: 160 and 189 are full-length sequences of SEQ ID NO: 60 and 122, respectively; and SEQ ID NO: 161 is related to SEQ ID NO: 61 and encodes the same amino acid sequence.

Example 2

USE OF SUCROSE PHOSPHATE PHOSPHATASE TO DEPHOSPHORYLATE SUCROSE-6-PHOSPHATE

The *F. arundinacea* and *L. perenne* FaSPP and LpSPP genes (SEQ ID NO: 7 and 8, respectively) share amino acid sequence identity with sucrose-6-phosphate phosphatase genes from other plant species (Lunn *et al.*, *Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). These genes were amplified by PCR using the primers given in SEQ ID NO: 191 and 192 to add an initiating methionine, and then cloned into the pET41a expression plasmid. These primers amplified nucleotides 263-1531 and 280-1548 for FaSPP and LpSPP, respectively. The resulting plasmids were transformed into *E. coli* BL21 cells using standard protocols, and protein expression was induced using IPTG.

The soluble recombinant protein was assayed for its ability to specifically dephosphorylate sucrose-6-phosphate (Suc-6-P) but not fructose-6-phosphate (Fru-6-P) using the procedure described by Lunn *et al.* (*ibid.*). The release of phosphate from Suc-6P and Fru-6-P was measured using the Fiske-Subbarow method of determining inorganic phosphate (SIGMA assay kit; Sigma, St Louis, MI), with the change in absorbance at 660 nm being proportional to the amount of phosphate released per unit time. As shown in Fig. 1, both the *Festuca* and *Lolium* SPP enzymes dephosphorylated Suc-6-P but not Fru-6-P, whereas control pET41 extract had no activity on either substrate.

20

Example 3

PEROXIDASE ACTIVITY OF GRASS ENZYMES DEMONSTRATED BY THEIR ABILITY TO OXIDIZE

2,2'AZINO-BIS.3-ETHYLBENZYLTHIAZOLINE-6-SULFONIC ACID (ABTS)

25

A number of *L. perenne* or *F. arundinacea* genes (SEQ ID NO: 48 – 54) share amino acid identity with peroxidase genes from other plant species (Hiraga *et al.*, *Plant Cell Physiol.* 42:462-468, 2001). The putative amino acid secretion signal sequence was identified by signalP analysis of the *Lolium* and *Festuca* sequences and homology to known peroxidase proteins. Primers were designed to amplify DNA representing the mature protein (minus signal sequence; Table 3.). These genes were amplified by PCR to add an initiating methionine and then cloned into the pET25b expression plasmid. The resulting plasmid was

transformed into *E. coli* AD494 (DE3) pLysS cells using standard protocols, and protein expression was induced using IPTG.

TABLE 3

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO:	DNA bp amplified	Protein codons
50	112	FaPER3	193 194	156-1077	24-326
52	114	LpPER5	195 196	120-1052	35-344

5

The insoluble recombinant protein was solubilized and re-folded following protocols described for several recombinant *Arabidopsis* peroxidases (Teilum *et al.*, *Protein Exp. and Purif.* 15:77-82, 1999). The insoluble inclusion bodies within *E. coli* were isolated from
 10 lysed cells by standard protocols and the recombinant protein solubilized in 8M urea. The solubilized peroxidase protein was refolded to gain active enzyme by diluting urea to 2M with 5μM Heme, 0.25mM Glutathione reduced, and 0.45mM Glutathione oxidized, pH 8 (20mM Tris-HCl). The refolded protein was used directly to assay peroxidase activity.

Peroxidase activity was measured by incubating recombinant peroxidase with pre-
 15 mixed ABTS/H₂O₂ liquid substrate (Sigma, St Louis, MI) and measuring ABTS oxidation by the increase in absorbance at 405nm. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control. The results provided in Fig. 2 show that FaPER3 and LpPER5 (SEQ ID NO: 50 and 52, respectively) had similar activity to that of horseradish peroxidase in these assays.

20

Example 4

USE OF GRASS FRUCTOSYLTRANSFERASE GENES TO SYNTHESIZE FRUCTANS

Transformation of *N. benthamiana* plants with fructosyltransferase genes

25 Sense constructs containing a polynucleotide including the coding region of fructosyltransferase genes isolated from *L. perenne* Lp1-SST and Lp6SFT1 (SEQ ID NO: 125 and 126, respectively) were inserted into a pART27 derived binary vector and used to

transform *A. tumefaciens* LBA4404 using published methods (*see, An et al.*, "Binary Vectors," in Gelvin and Schilperoort, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR). The primers px17 (SEQ ID NO: 207) and px18 (SEQ ID NO: 208) were used to confirm the presence of the Lp1-SST construct; whereas the primers px19 (SEQ ID NO: 209) and px 20 (SEQ ID NO: 210) were used to confirm the presence of the Lp6-SFT-1 construct.

The *A. tumefaciens* containing the sense gene constructs were used to transform *N. benthamiana* leaf discs (Burow *et al.*, *Plant Mol. Biol. Report* 8:124-139, 1990). Several independent transformed plant lines were established for the sense construct for each fructosyltransferase gene. DNA was isolated from transformed plants containing the appropriate fructosyltransferase gene construct using the QIAGEN DNAeasy Plant Mini Kit (Qiagen, Valencia, CA). Presence of the fructosyltransferase gene was verified using PCR experiments as shown in Figs. 3 and 4. For the Lp6-SFT1 gene, the forward and reverse primers given in SEQ ID NO: 197 and 198 were used, respectively. These primers amplify nucleotides 1572 - 1980 of the Lp6-SFT1 gene which corresponds to a 406 base pair fragment. For Lp1-SST, the forward and reverse primers given in SEQ ID NO: 199 and 200 were used, respectively. These primers amplify nucleotides 1332 - 1740 of Lp1-SST, corresponding to a 414 base pair fragment.

Effects of fructosyltransferase genes on fructosyltransferase concentration in transformed plants

Fructans are not normally found in *N. benthamiana* plants; hence, if introduction of the sense fructosyltransferase constructs was successful, it should be possible to extract fructans from the transformed plants. The concentration of fructosyltransferase in the transformed plants was determined using the Fructan Assay Kit (Megazyme International Ireland Ltd, Wicklow, Ireland). Briefly, 300 mg of leaf material from the independent transformed plant lines containing the fructosyltransferase sense constructs were extracted individually at 80 °C with 1 ml 80% ethanol, followed by two 1 ml extractions with water. The ethanol and water extracts were combined and frozen overnight at -20 °C. Extracts were centrifuged at 20,000 g to pellet chlorophyll. Clarified extracts were treated with 1%

PVP-40 to precipitate phenolic compounds. These extracts were then reduced in volume by rotary evaporation.

Fructan levels were determined in these extracts using the Megazyme Fructan Assay kit. Briefly, sucrose, starch and reducing sugars are removed from the plant carbohydrate extracts by using sucrase, β -amylase, pullulanase and maltase, and then converting the resulting reducing sugars to sugar alcohols. The remaining fructans are hydrolyzed with fructanase and the reducing sugars produced (glucose and fructose) are measured by the 4-hydroxybenzoic acid hydrazide (PAHBAH) reducing sugar method. The final extracts are assayed for absorbance at 410 nm. As shown in Fig. 5, fructans could be detected in both the Lp1-SST and Lp6-SFT-1 transgenic lines. Fructan levels were highest in lines 07, 09 and 12 for Lp1-SST, and lines 05 and 12 for Lp6SFT-1.

Example 5

USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *F. arundinacea* gene (FaSPS-N; SEQ ID NO: 9) has been identified that shares amino acid sequence identity with sucrose phosphate synthase (SPS) from other plant species. SEQ ID NO: 7 and 8 are also SPS sequences, with SEQ ID NO: 7 being a *Lolium perenne* homologue of SEQ ID NO: 9. The FaSPS-N was cloned into the pcDNA3 mammalian expression plasmid and the resulting plasmid transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA).

Cell lysates from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay. In this assay, mammalian cell extracts were tested for their ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Following the synthesis reaction, hexoses were converted to sugar alcohols by boiling in the presence of 30% KOH. The sucrose synthesized was detected by the addition of 1.4 % anthrone reagent in H_2SO_4 and incubating at 40 °C for 20 min. The change in absorbance at 620 nm is relative to sucrose in the reaction (Botha and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000). In these experiments, introducing FaSPS-N alone into mammalian cells produced a sucrose synthesis activity that was not detected in non-transfected cells (Fig. 6).

A known cofactor for SPS is SPP. To test whether SPP is required for SPS activity, the *L. perenne* LpSPP gene (SEQ ID NO: 8) was cloned into the pcDNA3 mammalian expression plasmid. Both the FaSPS-N and LpSPP plasmids were co-transfected into 293T mammalian cells using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA). Cell lysates
5 from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay as described above. As shown in Fig. 6, adding SPP did not significantly enhance or alter the sucrose synthesis activity of the cell extracts.

Example 6

10 USE OF SOLUBLE SUCROSE SYNTHASE ENZYMES TO CLEAVE SUCROSE

A *F. arundinacea* gene (FaSUS-1; SEQ ID NO: 13) was identified that shared amino acid sequence identity with soluble sucrose synthase enzymes (SUS) from other plant species. The FaSUS-1 gene was cloned into the pcDNA3 mammalian expression plasmid,
15 which was transiently transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen Carlsbad, CA). Transfected cells were grown for several days before harvesting (by scraping cells in a sucrose synthase buffer). Harvested cells were frozen on dry ice and freeze-thawed twice before pelleting cell debris by centrifugation. The resulting supernatant (cell lysate) was deionized on G25 spin
20 columns and then used in a sucrose cleavage assay as described by Sebkova *et al.* (*Plant Physiol.* 108:75-83, 1995). In these assays, the cell lysates were tested for their ability to cleave sucrose in the presence of UDP to produce fructose and uridine 5'-diphosphoglucose. Following a 30 min incubation at 30 °C, the enzyme activity was stopped by boiling the tubes for 1 min. Both NAD and UDP-glucose dehydrogenase were added and the change in OD at
25 340 nM (production of NADPH) was measured. As shown in Fig. 7, significantly higher levels of sucrose cleavage were observed in cells transfected with FaSUS1 construct than in non-transfected control cells.

Example 7USE OF ACID INVERTASES TO CLEAVE SUCROSE

A number of acid (vacuolar and cell wall) invertase genes from *L. perenne* and *F. arundinacea* (SEQ ID NOS: 17, 19, 21, 23 and 135-141) were identified that share amino acid sequence identity with acid invertases from other plant species (Unger *et al.*, *Plant Physiol.* 104:1351-1357, 1994; Goetz and Roitsch, *J. Plant Physiol.* 157:581-585, 2000). These sequences were analysed by SignalP and homology to identify signal regions and propeptide sequences, and primers were designed to amplify the DNA sequence encoding the mature protein (Table 4).

TABLE 4

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO	DNA bp amplified	Protein codons
17	79	LpCWINV1	201 202	137-1803	38-583
19	81	FaCWINV4	203 204	134-1912	26-597
25	87	LpSINV1	205 206	387-2124	104-668

The PCR fragments were cloned into pPICZ α A vectors for expression in methylotrophic yeast *Pichia pastoris* (EasySelect™ *Pichia* Expression Kit, Invitrogen, Carlsbad, CA). The sequences were cloned in frame with the α -mating factor for secretion of the recombinant invertase protein into liquid media, following similar methods described for the expression of barley 6-SFT and fescue 1-SST in *P. pastoris* (Hochstrasser *et al.*, *FEBS Letters* 440:356-360, 1998; Lüscher *et al.*, *Plant Physiol.*, 124:1217-1227, 2000). The media was concentrated 10 fold by Vivaspin 30 kDa spin column (VivaScience, Hannover, Germany) to concentrate recombinant protein and used directly to assay invertase activity. Recombinant protein was assayed with 100mM sucrose in 500 μ l phosphate buffer pH5.0, at 30 °C for 1 hour. Release of glucose by invertase activity was measured using a glucose HK assay kit (Sigma, St Louis, MI). Fig. 8 shows the glucose released by invertase activity in terms of glucose concentration in the assay mix. As shown in Fig. 8, invertase activity was observed for the vacuolar invertase (LpSINV1; SEQ NO: 25) and the two cell wall invertases

(LpCWINV1 and FaCWINV4; SEQ NO: 17 and 19, respectively) but not for an empty vector (pPICZalphaA) control.

Example 8

5

USE OF TANNIN GENES TO MODIFY TANNIN BIOSYNTHESIS

Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 5.

10

TABLE 5

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	<i>tt3</i>	5
Chalcone synthase	CHS	<i>tt4</i>	5
Chalcone isomerase	CHI	<i>tt5</i>	3
Flavanone 3- β -hydroxylase	F3 β H	<i>tt6</i>	3

Over-expression of the maize genes for CHS, CHI and DFR has been shown to complement the *Arabidopsis tt4*, *tt5* and *tt3* mutants, respectively, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001).
 15 Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

Sense constructs containing a polynucleotide including the coding region of tannin genes isolated from *L. perenne* or *F. arundinacea* LpCHS, LpCHI, LpF3 β H, LpDFR1, FaCHI and FaF3 β H (SEQ ID NO: 157, 55, 161, 159, 56 and 62, respectively) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," in Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the
 20 binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the
 25 primer pairs described in Table 6.

TABLE 6

Gene	SEQ ID NO:	Transparent testa line	Forward Primer SEQ ID NO:	Reverse Primer SEQ ID NO:
LpCHS	157	<i>tt4</i>	211	212
LpCHI	55	<i>tt5</i>	213	214
LpF3 β H	161	<i>tt6</i>	217	218
LpDFR1	159	<i>tt3</i>	215	216
FaCHI	56	<i>tt5</i>	213	214
FaF3 β H	62	<i>tt6</i>	217	218

5 The *A. tumefaciens* containing the sense gene constructs are used to transform *Arabidopsis* by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998). Several independent transformed plant lines were established for the sense construct for each of the tannin genes. Specifically, LpDFR1 constructs were transformed into *Arabidopsis tt3* mutants, LpCHS constructs were transformed into *Arabidopsis tt4* mutants, LpCHI and
10 FaCHI constructs were transformed into *Arabidopsis tt5* mutants, and LpF3 β H and FaF3 β H constructs were transformed into *Arabidopsis tt6* mutants. Several independent transformed plant lines were established for the construct for each of the tannin genes. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

15 The presence of cyanidin in the FaCHI transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 *g* for 20 min. Any remaining chlorophyll is removed through
20 a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

SEQ ID NOS: 1-218 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

5 All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied
10 considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) SEQ ID NO: 1-62 and 125-162;
 - (b) complements of SEQ ID NO: 1-62 and 125-162;
 - (c) reverse complements of SEQ ID NO: 1-62 and 125-162; and
 - (d) reverse sequences of SEQ ID NO: 1-62 and 125-162;
2. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of SEQ ID NO: 1-62 and 125-162;
 - (b) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-62 and 125-162;
 - (c) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-62 and 125-162; and
 - (d) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-62 and 125-162,wherein the polynucleotide encodes a polypeptide having substantially the same functional properties as a polypeptide encoded by SEQ ID NO: 1-62 and 125-162.
3. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.
4. A kit comprising a plurality of oligonucleotide probes or primers of claim 3.
5. A genetic construct comprising an isolated polynucleotide of any one of claims 1 and 2.

6. A transgenic cell comprising a construct according to claim 5.
7. A construct comprising, in the 5'-3' direction:
 - (a) a gene promoter sequence;
 - (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide encoded by a polynucleotide of any one of claims 1 and 2; and (2) a polynucleotide comprising a non-coding region of a polynucleotide of any one of claims 1 and 2; and
 - (c) a gene termination sequence.
8. The construct of claim 7, wherein the polynucleotide is in a sense orientation.
9. The construct of claim 7, wherein the polynucleotide is in an anti-sense orientation.
10. A transgenic plant cell comprising a construct of claim 7.
11. A plant comprising a transgenic plant cell according to claim 10, or fruit or seeds or progeny thereof.
12. A method for modulating one or more of the lignin composition, fructan composition and tannin composition of a plant, comprising stably incorporating into the genome of the plant at least one polynucleotide of any one of claims 1 and 2.
13. The method of claim 12, wherein the plant is selected from the group consisting of grasses.
14. The method of claim 13, wherein the plant is selected from the group consisting of: *Lolium perenne* and *Festuca arundinacea*.

15. The method of claim 12 comprising stably incorporating into the genome of the plant a construct of claim 7.

16. A method for producing a plant having one or more of altered lignin composition, altered fructan composition and altered tannin composition, comprising:

- (a) transforming a plant cell with a construct of claim 7 to provide a transgenic cell; and
- (b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

17. A method for modifying the activity of a polypeptide involved in a lignin, fructan or tannin biosynthetic pathway in a plant comprising stably incorporating into the genome of the plant a construct of claim 7.

18. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 63-124 and 163-190.

19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

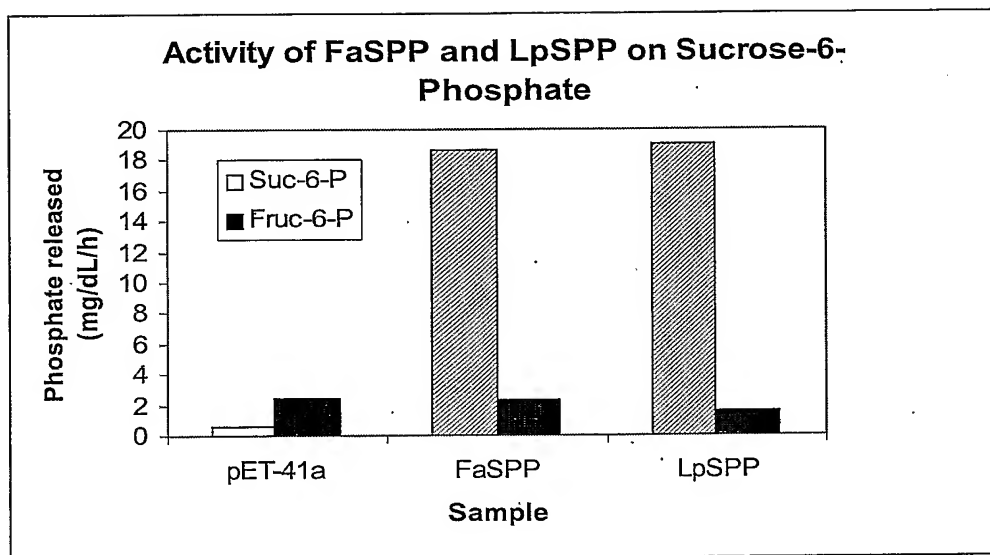
- (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 63-124 and 163-190;
- (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 63-124 and 163-190; and
- (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 63-124 and 163-190

wherein the polypeptide has substantially the same functional properties as a polypeptide of SEQ ID NO: 63-124 and 163-190.

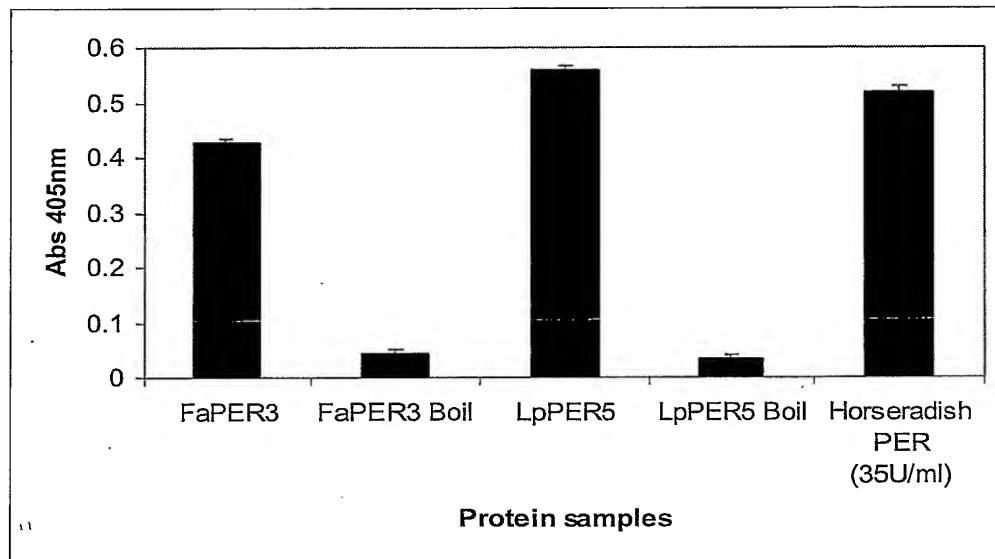
20. An isolated polynucleotide that encodes a polypeptide of claim 18.

21. An isolated polypeptide encoded by a polynucleotide of any one of claims 1 and 2.

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**Figure 1.**

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**Figure 2.**

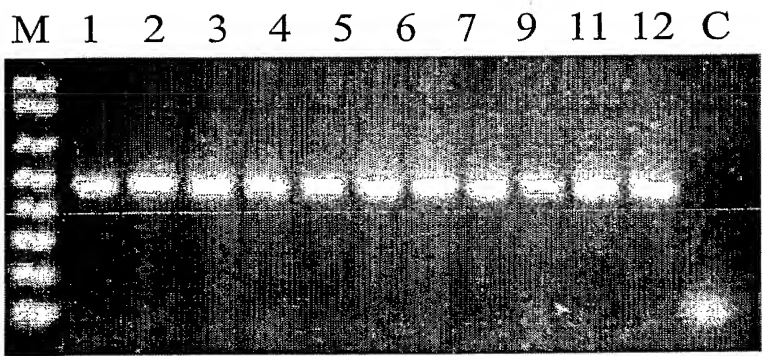


Figure 3.

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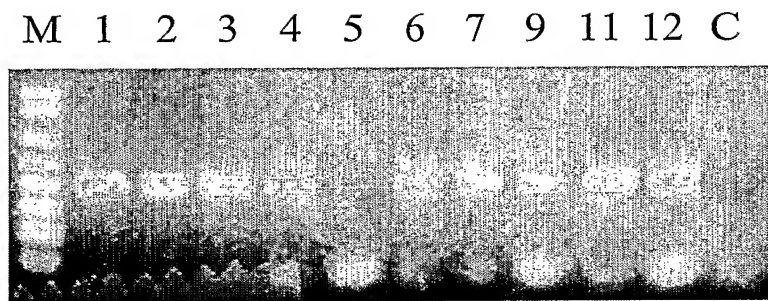


Figure 4.

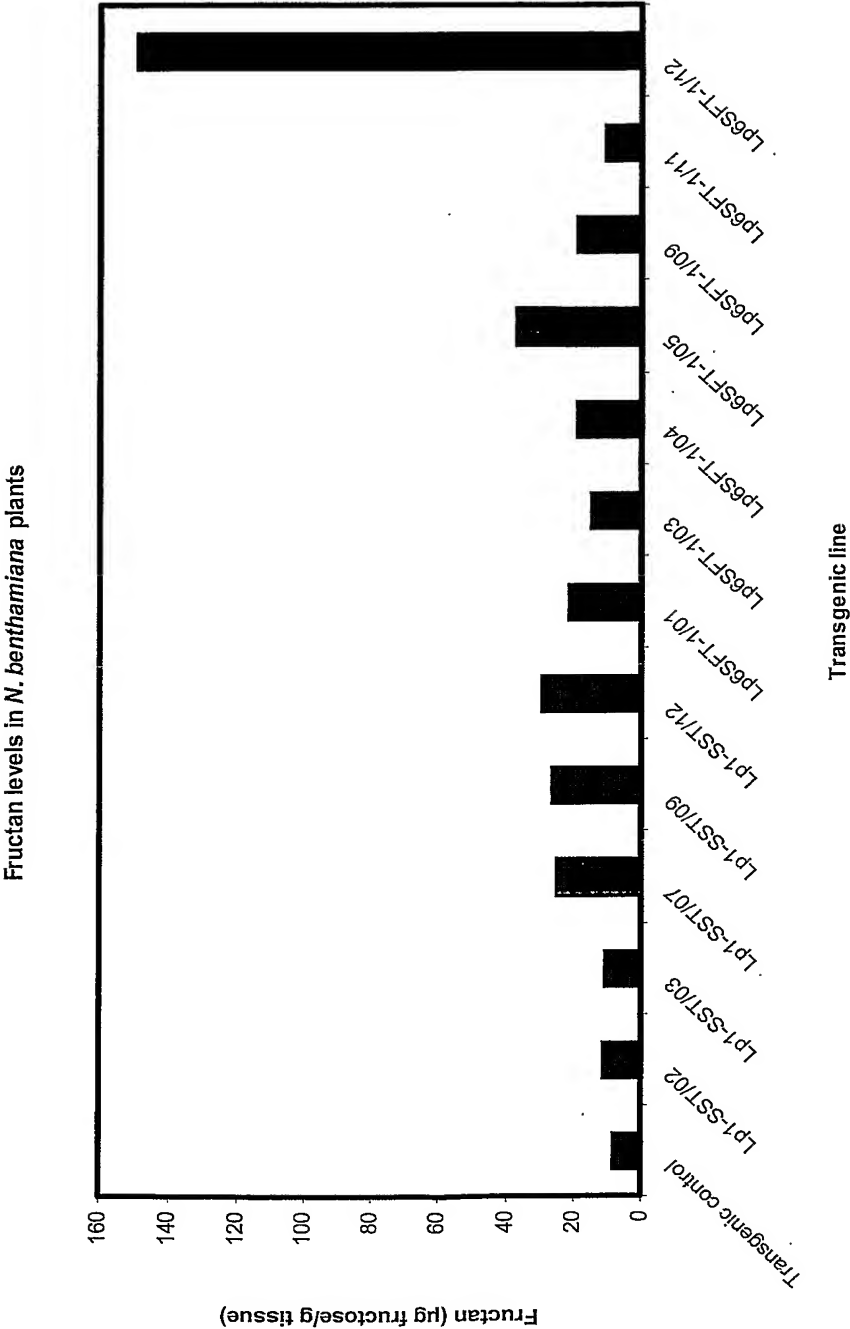
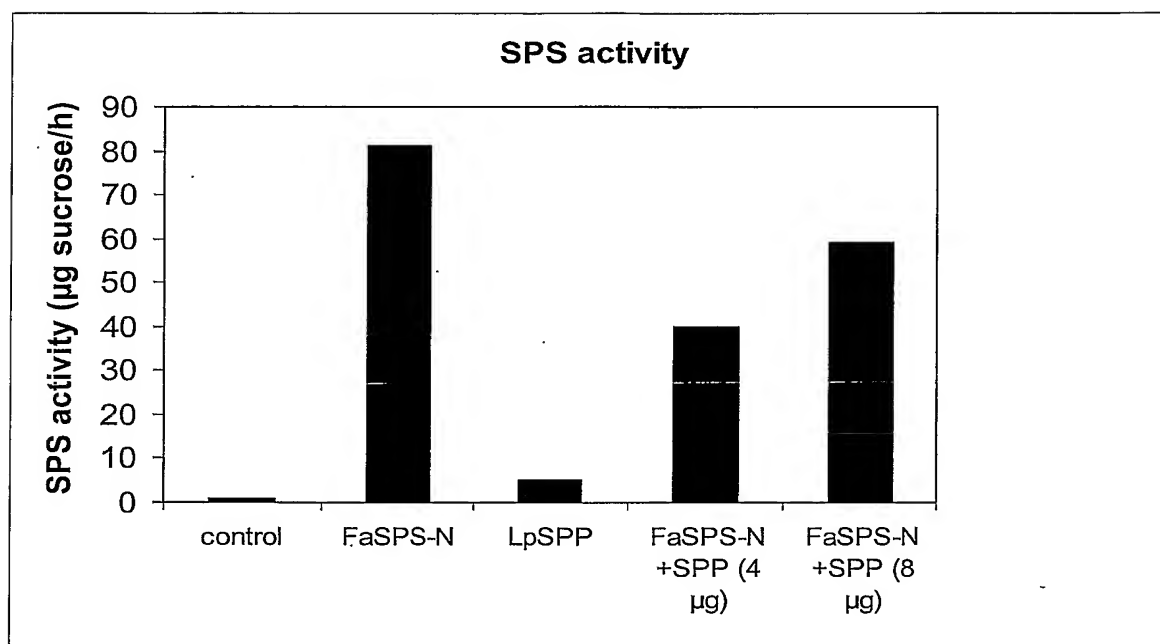
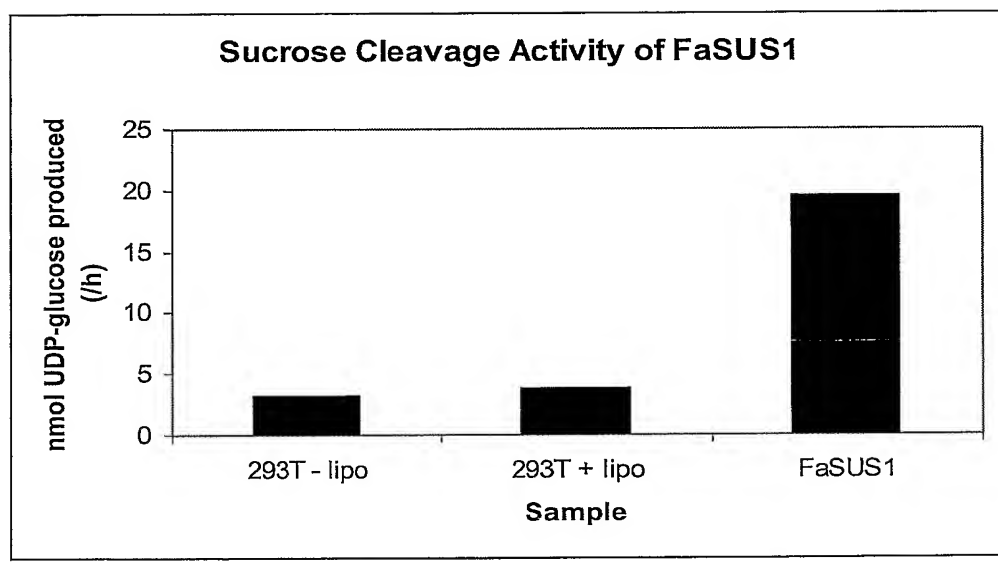


Figure 5.

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**Figure 6.**

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**Figure 7.**

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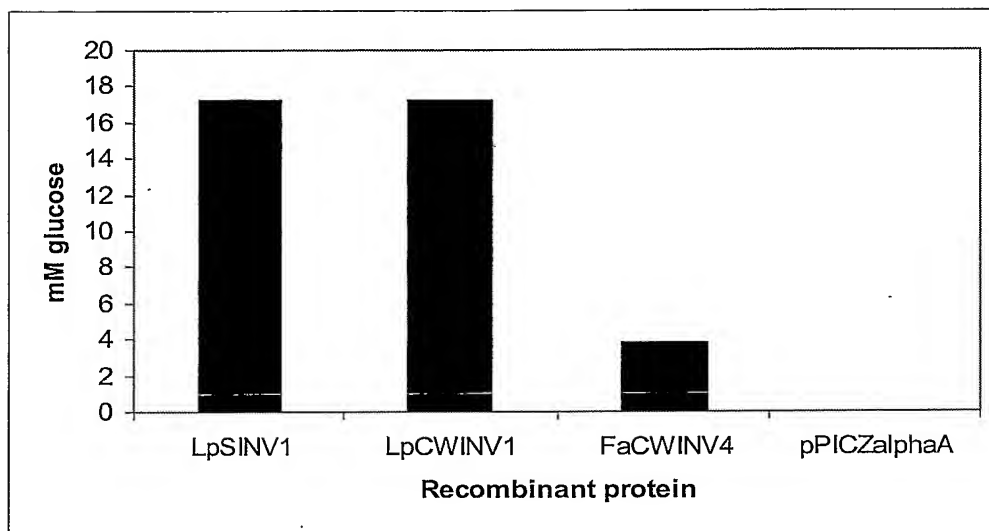


Figure 8.

SEQUENCE LISTING

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<211> 1778

<212> DNA

<213> Lolium perenne

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<211> 3629

<212> DNA

<213> Festuca arundinacea

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<213> *Lolium perenne*

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<213> Lolium perenne

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<212> DNA

<213> Festuca arundinacea

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<212> DNA

<213> Lolium perenne

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<210> 22

<211> 1760

<212> DNA

<213> Lolium perenne

<400> 22

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<210> 23

<211> 2059

<212> DNA

<213> Festuca arundinacea

<400> 23

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<210> 24
<211> 2167
<212> DNA
<213> *Lolium perenne*

<400> 24
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<210> 25
<211> 2138
<212> DNA
<213> *Lolium perenne*

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<210> 26

<211> 1768

<212> DNA

<213> *Lolium perenne*

<400> 26

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<210> 27
 <211> 1855
 <212> DNA
 <213> *Lolium perenne*

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 ggggataaaa gttttgtcta cgttttcttt tacgctactc tctccattga ggagtacaat 1800
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<210> 28
 <211> 2041
 <212> DNA
 <213> *Lolium perenne*

<400> 28
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 ccgcgggagc ttggtttccg gtcgaagctc ccggacatcg agatcccga ccaactgacg 180
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<210> 29

<211> 1934

<212> DNA

<213> Festuca arundinacea

<400> 29

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tgttccggtc	caagctccc	gacatcgaga	tcccgaacca	cctgacgctg	caggactact	180
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gcctgggggt	ccgcaagggc	gacgtcgtca	tggcgctgct	ccgcaactgc	ccggagtctc	360
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aatgttctta	atataaatgg	aaattaatac	atatagaagg	gctgattctt	tttactagat	1860
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<210> 30

<211> 2014

<212> DNA

<213> Lolium perenne

<400> 30

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ccaaatgggg	aaagaaacta	cgggagggga	tcatattatt	cttgaggag	atatcagttt	1920
gttgattcgc	cctgcttggtg	taatgttgat	aaaatgaaat	gatagaatag	atgtgttggt	1980
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<210> 31

<211> 2073

<212> DNA

<213> Festuca arundinacea

<400> 31

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ctcgtagatc	attaccatgg	ggtctgtgcc	ggaggagtca	gtggtagccg	cggccgtggc	180
ggagacgggtg	ttccggtcga	agctccctga	catcgagatc	aacaacgagc	agacgctgca	240
gagctactgc	ttcgagaaga	tggccgaggt	cgcatcccg	ccctgcatca	tcgacgggca	300
gacggggcgc	tcctacacct	acacagaggt	ggagtccctg	acccgtcgcg	ccgcggcggg	360
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caa	atg	ggg	ga	ggg	gtac	atgat	cagat	tatt	ctt	gca	ggag	atatca	1920
gtt	gtt	ggg	tgc	ccct	gtc	tgt	gta	aat	gata	aaat	gatata	atagat	1980
tg	ttt	tatt	ttt	gac	cat	gta	aga	acaa	ggct	ggg	att	ttact	2040
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<210> 32

<211> 1798

<212> DNA

<213> *Lolium perenne*

<400> 32

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gat	gg	aggtc	ctc	ctc	ctgg	aga	aagg	ccct	act	ggg	gctc	ttc	gcg	gcg	cggt	gctggc	120
cat	gc	ccgtc	gc	ga	agctcg	cc	ggca	aagcg	ctt	ccgc	ctc	ccg	ccc	ggcc	cct	ccgg	180
cccc	atc	gctc	gg	ca	actggc	tcc	aggt	cg	gc	ac	ctg	aacc	accg	ca	acct	gat	240
cat	gc	gaa	cg	gttc	gggg	aggt	gttc	ct	gct	ccg	catg	gg	cat	ccg	ca	acct	300
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<210> 33

<211> 1775

<212> DNA

<213> *Festuca arundinacea*

<400> 33

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ag	cg	tcc	g	gtg	tcg	cg	a	tcg	tcg	gtc	ca	ag	at	ccg	c	tg	ag	180
g	ccg	gg	cccc	at	cccc	gt	gc	ccat	ctt	cg	ca	act	gg	ctg	cag	gt	cg	240
cc	acc	gca	ac	ctg	ggc	gg	cgga	tgg	ccc	gcaa	gtt	cg	ggg	ag	gt	gt	ctc	300
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gc	agg	acatg	gt	gtt	ccag	g	tgt	ac	gg	cgga	cc	act	gg	cg	c	gg	at	480
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ca	ac	gtc	ctc	tac	at	catcg	aga	ac	at	ca	caa	cg	tc	gc	cg	cg	g	1020
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<210> 34

<211> 1323

<212> DNA

<213> *Lolium perenne*

<400> 34

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tgagggtgta	ggcgagggtg	tggaggtcgg	gccggagggtg	agcaagtaca	gcgtcggcga	300
tgtggtcggc	gtgggggtga	tcgttgggtg	ctgccgcgac	tgccggccgt	gcaaggccaa	360
cgttgagcag	tactgcaaca	agaagatctg	gtcgtacaac	gacgtctaca	ccgacggaaa	420
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aaa						1323

<210> 35

<211> 1313

<212> DNA

<213> *Festuca arundinacea*

<400> 35

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cgggtggggc	gccagggaca	ccaccgggtca	cctctccccc	tacacgtaca	ccctcaggag	180
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ggtaggcgag	gtggtggagg	tcgggcccga	ggtgagcaag	tacagcgctg	gcgacgtggt	360
tgggctcggg	gtgatcgctg	ggtgctgcca	cgactgcggg	ccgtgcaagg	ccaacgttga	420
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gcgataattt	ccgtgacata	tgctcctcaa	ctcggtgcag	tacatgattg	tgacctgtgt	1260
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<210> 36

<211> 1059

<212> DNA

<213> *Lolium perenne*

<400> 36

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gccagcgggtg	ccgagcaggt	cacccgccac	tccgaggctg	ggcacaagag	cctgctccag	180
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atgaagcagc	tccgcgagga	caccgcgaac	cacccatgga	acctgatgac	cacgtoggcg	300
gacgagggcc	agttcctcaa	cctgctcatc	aagctcatcg	gcgccaagaa	gaccatggag	360
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ttctgtatct	tcttggaaac	aaatattgtc	cctttatgta	cgtatatcaa	atthtatatcc	1020
agacaaataa	tattactcct	ataaaaaaaaa	aaaaaaaaaa			1059

<210> 37

<211> 1063

<212> DNA

<213> *Festuca arundinacea*

<400> 37

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aatttatatc	cagacaaata	atattactcc	tataaaaaaa	aaa		1063

<210> 38
 <211> 1333
 <212> DNA
 <213> *Lolium perenne*

<400> 38						
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gaacacccgt	cccatattaa	ctatcaacat	gacagtcgtc	gaggtcttag	ctgccggcga	180
cgccgcgcgc	gccgcggtgg	cgccggccgc	cggaacggg	cagaccgtgt	gtgtgaccgg	240
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caagggcacc	gtcaggaacc	cagacgaccc	gaagaacgcg	cacctgaggg	cgctcgacgg	360
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gcgcatcgac	ggctgccacg	gctcttcca	caccgcatcc	ccagtcaactg	acgaccccga	480
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<210> 39
 <211> 1237
 <212> DNA
 <213> *Festuca arundinacea*

<400> 39						
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<210> 40
 <211> 1429
 <212> DNA
 <213> *Festuca arundinacea*

<400> 40
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<210> 41
<211> 1457
<212> DNA
<213> *Lolium perenne*

<400> 41
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<210> 42
<211> 1452
<212> DNA
<213> *Festuca arundinacea*

<400> 42

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<211> 1440

<212> DNA

<213> Lolium perenne

<400> 43

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<211> 2102

<212> DNA

<213> Lolium perenne

<400> 44

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<211> 2051

<212> DNA

<213> Festuca arundinacea

<400> 45

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 <211> 2461
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 <213> *Lolium perenne*

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 <211> 2596
 <212> DNA
 <213> *Festuca arundinacea*

<400> 47

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<211> 1301

<212> DNA

<213> Festuca arundinacea

<400> 48

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acagggattc	agattcagtc	atctctcctt	cgcatggtct	atctgtttcc	cacagaaaat	1200
aaggatataa	taatactgta	taatcctgta	aaaaaaggaa	acgatactgt	atagttgtgc	1260
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<210> 49

<211> 1236

<212> DNA

<213> *Lolium perenne*

<400> 49

gagatggctt	cttcttcctc	ccccctttct	cgggtctccc	agctagccgt	caaggcgacg	60
gtcctggcgg	ccgtctgcct	cctcctccac	ggcggaggcg	ggagttagcg	atcggcgggc	120
gagctgtgcg	tgagctacta	cgaccacacg	tgctccggacg	cgtaacaagat	cgtagcagggg	180
gtgctgggtg	aggctcacia	gtcggaccgc	cgcatcttcg	ccagcctcat	ccgcctccat	240
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gccaaccaat	gtacgtaaga	ttatgtgcat	gctttgatcc	cacaagtgca	atgaagtga	1200
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<210> 50

<211> 1205

<212> DNA

<213> *Festuca arundinacea*

<400> 50

gcaagcttcc	ctcgattagc	taccttgtct	agccaccgtc	gtccttgac	agccaaggaa	60
gaagcaaagc	tattttggctt	ctaacaatgg	cgacgagggg	tgatcatggtg	gcgctgctgc	120
tcgcggcggg	ggcggcgtct	tgcgctcatg	cacagctgca	cgagaagttc	tacagttagt	180
cgtgccccag	cgtggaggac	gtcgtccgga	aggagatggt	catggcgcta	tccttcgcgc	240
caagcctcgc	cgcgccgctc	ctcaggatgc	acttccacga	ctgcttcgct	agggggtgcg	300
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agttcttcgc	cgactttgcc	gtctccatgg	taaagatggg	caacaccgac	gtgctcactg	1020
gaagccaggg	cgagatcagg	aagaagtgtc	ccgtggtgaa	ccattagtta	gccctggaa	1080
taccggttgg	cataccaacc	cttttgattt	gtgacctgt	ttttttctg	tgtagattat	1140
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aaaaa						1205

<210> 51
 <211> 1382
 <212> DNA
 <213> *Lolium perenne*

<400> 51
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 ggccgcggcc accaagatca gtgtctccact accgccgctg gccaagggcc tgaacttcga 180
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 cgctctcctc gccaaaggcct gcggcgccgt cgtctcctgc gccgacatcg ccgccctggc 480
 cgcgcgcgac tcctgtcacc tcgccggcgg gccgcactac cccttcccgc tcggccgcgcg 540
 cgacgggctc gcccccgcga acctcaccac catcctcaac gccctcccgc caccgagctc 600
 caacgtcacc acctcctcga gattcctcgc caagatcagc ctgcagccca acgacctcgt 660
 cgcgctatcc ggccgcgaca cgctcggcat cgcgcactgc acctccttcc agggagcgct 720
 cttcccgagc aacgacgtca cctcaacaa gtggttcgag tcgcagctca ggctcacctg 780
 cccggcgctc aacaccgaca acaccacaa caacgacatc cgcaccccca acgtcttcga 840
 caacaagtac tacgtcgacc tgctcaaccg ccagggactc ttacacctcg accaggacct 900
 gcacaccgac gccaggacca agcccaccgt caccagggtc gccgtcgacc agggccgctt 960
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 ccagggacag atacgcaacg actgctccgc gcccaacaaa ggccgcacca acgacgacct 1080
 gccgtggtcc gtgctcgaga ccgtcaccga ggccgcccag agcttggtgt ttagatatatg 1140
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 ttagctttta ttagcgagcc gtgtggtaat ggtttgggtc ttgagagcca cagttgatgc 1260
 atgtgtgttt agtttcttga gaaactcgac cagtttaata atcacgagat ggtttttggt 1320
 gtgtcgaatg acgactagaa aattgagatg aatatttgat gttattttca ataaaaaaaa 1380
 aa 1382

<210> 52
 <211> 1261
 <212> DNA
 <213> *Lolium perenne*

<400> 52
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 aaggttctgg gctgtccgtc gggttctaca agaagttgtg tccgaaggcg gagaaggctg 180
 tccggcgaaac tgtcaccaag gcctttgaga aggagcctgg caccocggcc gacatcatcc 240
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 ccttcacgga ccgcctctac aacttctccc agggcgggcg gctgaccacg gaccctgcgc 720
 tgccggcggc atacgccgcy ctgctgaagg agaagtgcc gccggagaca gcggcgacga 780
 acgacaccac catggtgcag ctgcagcagc tgacgcccgt cgtgatggac aaccagtact 840
 acaagaacct gcttgccggc accgtgccgc tcggctccga cgtagcgctc atggagagcc 900
 ccgacacggc ggccgctcgtc gagctctacg cccgcgagcc cggcgagtac tgggccaagc 960
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 agatccggct caactgctcc aaggtgaact agtatataac cggttgctgc gtttgcctct 1080
 gtactatatg tttgggaaag atgacgatac acgttcttct tttgtgttaa tgtttttct 1140
 ttcatttgtt ttcatatggt ggtgagaaat atatacacat ttgtttgcgt cataaactgt 1200
 aaagcttaca cagcatgcat aaaagcatct atatcattcc atttgagttg taaaaaaaaa 1260
 a 1261

<210> 53
 <211> 1059
 <212> DNA
 <213> *Lolium perenne*

<400> 53
 acgaggggaga actactacgg gtcttcttgt cccaccgcgc ttctcaccat caggactgtc 60
 gtgacgacgg cgggtgctgct ggaccaccgc atgggcgctt ctcttctccg gctccacttc 120
 cactgactgct ttgtgcaagg gtgacgacgg tccgttctgc tggatgacac ggccggcttc 180
 accggcgaga agggggccgg gccgaacgcc ggggtcgctgc gcggtctgga ggtgatcgac 240
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 ggaaggaggg acgccaccac agcaagcgcg tcacttgcta gtagtgacct cccaggcccc 420
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 tgtacactgc ctattttatt cctgtccttg tgtcccgctc ttgttatatt acatccataa 1020
 tccatgttaa gatggtggca ttggttttaa aaaaaaaaaa 1059

<210> 54

<211> 1266

<212> DNA

<213> Festuca arundinacea

<400> 54
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 tctggccgcc acggcgggcgt cggcgacgct gtogtcaacg ttctatgaca cgtcgtgccc 180
 caggcccttg gccaccatca agagcggcgt ggccggccgc gtgagcagca acccccgcat 240
 ggggtcgctc ctgctcaggc tgcacttcca cgaactgctt gttaatggct gtgacgcgtc 300
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 cgtggacatg gtacgctct cggcgcgca caccatcggg cggcgcgagt gccagaactt 660
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 atatacgtgc agctcaaaat tattcatgca cctctacaca tgtaactatc gaattctctc 1200
 atgcaaaggc ataaagaatt acttcaatat atacaactac aactaccatt attctcaaaa 1260
 aaaaaa 1266

<210> 55

<211> 1164

<212> DNA

<213> Lolium perenne

<400> 55
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 gcccaagtgc cctggcttgg ccggtcggca ctccccctcat cccctggctc accctcccc 120
 tcaggctcct ctctctctcc cctggccctg gaggcagtcg gtcggatctg gccggtcgcc 180
 ggagacgcgc tcggccgtcc actgctcgcc gccgctgcct tctagccact accgttcagc 240
 ctccagagcc aagcggcagt ctagcccaac agcaggagcg tagaatagtg ttacctcttg 300
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 ccgctcgttg ccgctccgcc gggcacagcc cagcgccact tcctcgccgg cgcagggtgtg 420
 cgagggatgg agctcggcgg caacttcatc aagttcacgg ccatcggcgt gtacctgcag 480
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cggacaccgt	caactgctggc	ttgtgtggtt	ggcgatgtcc	gttgttgaga	cgtcgtgttc	1080
cggagtttct	accgttgttt	tctgttgtgt	cgaggtgaac	cgtgctaact	tgaataaaga	1140
aaccgctgcc	caagaaaaaa	aaaa				1164

<210> 56

<211> 933

<212> DNA

<213> Festuca arundinacea

<400> 56

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ccgcggggca	cagcccacgc	gcacttcctc	gccggcgagc	gtgtgcgagg	gatggagctc	180
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cgcctcaccc	gcgcgcagta	ctccgagaag	gtgaccgaga	actgcgtcgc	ctactggaag	420
gccgtcggca	agtacacgga	cgctgaggcc	gccgcgctcg	acaagttcaa	ggaggccttc	480
aaggccgaga	gtttccctcc	cggcgcgctc	atcctcttta	cccactcccc	cgccggcgctc	540
ctcacccgtc	cgttctcgaa	agactcgctg	ttgccggagt	cgggcggcgt	ggcgatagag	600
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<210> 57

<211> 1531

<212> DNA

<213> Lolium perenne

<400> 57

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gccgcgcaga	tgaccgtgga	ggagggtagg	aaggcacagc	gggcgggagg	gccggcgagc	180
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gagaacccca	acatgtgcgc	gtacatggcg	cgtcgtctgg	acgcgcgcga	ggacatagtt	420
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accaccaccg	gcgagggaat	ggattggggc	gtcctctttg	gcttcggggc	cggcctcacc	1260
gtcgagaccg	ttgtctcca	cagcatgccc	attgcgctg	atgccaccgc	ttgatcgatg	1320
gttccatctc	ctgttatctg	ccacatcgat	ggatacctac	tactactacc	gccgcgcgcg	1380
ctgctatcca	aagtaatttg	tattgtattc	atgcatacct	ggtttgtatt	tggtgtagg	1440
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<210> 58
 <211> 774
 <212> DNA
 <213> Festuca arundinacea

<400> 58
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 cggcatgccg cccagcctgg tcaccgccct ggcactcatc acggggaacg aggcccacta 180
 ctcgatcctg aagcaggtgc agctgggtcca cctggacgac ctctgcgact ccattgaccta 240
 cctcttcgag caccgggacg ccaacggccg ctacatctgc tcctcccacg acaccacat 300
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 ggagaagggc ctgattccgc tcggagcggg aggggcaggc ggcccggcca gtgcagccgg 540
 caagctggga gctgttctcg tgggcgaagg tcaggcgatt ggtgctgaga cataagcgt 600
 agtgcattga cactaggctg gctacctcag acacattggt gagcgatgat tatgttcgtt 660
 aattctacta tcctatatatt cggttcagaa attgcattaa gagaaccctg taattggtgg 720
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<210> 59
 <211> 1211
 <212> DNA
 <213> Lolium perenne

<400> 59
 ggagacacca cacatggcga ctgaagccaa gggggagacg gtgctggtca ccggcgccag 60
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 cgccgtcctc aaccccgatg acaaggccga gacggaccac ctctcgcgc tcgccgctgc 180
 ggccggcgac gaggggcgca tccgcttctt cagggtgcgac ctctcgcgc gcgccgccat 240
 gctcgccgac gtgcccggat gctccggcgt gttccacctc gcctctccct gcaccgtcaa 300
 cctcgtcctc aacccccaaa aggagcttgc ggtgcccggc gtggagggca cgtcaaacgt 360
 cctgcgcgac gccaaaggag ctgggggagc gggcggggtg gtggtgacct cctccgtctc 420
 cgccctcgtc ccctgccggg ggtggccggc cggcgaggct ctgacgagc gctgctggac 480
 cgacatcgac tactgcgaca agaacggggt ttggtaccct gcttcaaagg cactggcgga 540
 gaaggcggga tggaaagttg cagaggagaa tggactggat gtggtgacgg tcaatccagg 600
 gacgggtttg ggcgagatga ttccgccaag gctcaatgcc agcatggcca tgtttcttcg 660
 ctactttgaa gggtgcaaa aggagtatgc agatttcttc atcgggccag tgcacgtgga 720
 agacgttgca ttagcccata ttctgctgta cgagaatccg tcagcatccg ggaggcacct 780
 ctgctgggag cccatctgtc actggagtggt ttctcgccgc aaagtgcgcg agctctaccc 840
 tgattacaaa gttccaaaat tccctgagga cacacagcct gggctggtga gggcgaaggc 900
 ggtgcccata aagctgatgg cgttgggttt gcagttcact cctcttgaga agatcatcag 960
 ggtgcccgtg gagagcctca agagcagagg atgcatcgcc tgatgattgg atcggtaggc 1020
 atgtcacctt tccgtcgtag gttcatgatc atccttggtg aaaaatgtgt tgtgtgtgt 1080
 ccagcccagt gcctaccag accatatact taccagtatg atttgtgcaa taacagccgg 1140
 ttgatgtacg gcatcacctg ccctacactt gggatgcgga tgctgtcaca ctgactccct 1200
 caaaaaaaaa a 1211

<210> 60
 <211> 1229
 <212> DNA
 <213> Lolium perenne

<400> 60
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 cgaagaaagg ttggacacct ttggaaacta ccagggtgcaa atgagaggct ccaacttgtg 180
 agagctgac tattggagga agggagcttt gacgatgctg taagggtttg tgagggtgtc 240
 ttccacattg cgtcgcctgt ccttgggaaa tctgattcca attgcaagga agcaacactc 300
 ggtctgcaa tcaatggtac cctcaacgtg ctaagatcct gcaagaagag tccatttctc 360
 aaaagggttg ttctcacatc ttcatcatcc gcggttaagg ttagggatga aactcagcag 420
 ccagaaactgt tatgggatga aacgacatgg agctctgtgc cactctgtga aaagctacag 480
 ctatggtatg ccctggcaaa ggtattttgca gagaaagcag cattggactt tgccaaggag 540
 aataacattg accttgtgac agttcttcca tcattcgtaa ttggaccag tttatcccat 600
 gaattgtgca ctactgcttc agatatacctt ggcttacttc aaggtagcac agacaggttc 660
 actttgtacg gaaggatggg atatgttcac atcgatgatg ttgcccggag ccacattcta 720

gtgtacgaaa	caccggaggc	aactggcaga	tatctgtgca	gctcagtgg	tctggataac	780
aatgaattgg	ttggcttact	ggcaaaacag	tttccagtat	tccccattcc	aaggaggctc	840
aagaaccctt	atggaaagca	ggcataccag	ctagacacat	ccaagctcca	ggggctgggt	900
ctcaagtcca	aaggagtcca	ggagatgttt	aacgactgcg	tcgaatcgct	gaaagatcag	960
ggccatttgc	tggagtggcc	gttgtgataa	cagagacagc	attgacaagc	catagccaaa	1020
cagcattgac	aagccatagc	caaacacatc	tcaactatgc	ctgaatcatg	tcagttctcg	1080
agtcatagat	tttttttttc	tcttcaaata	attcccatgt	actctcctta	ctataaccgaa	1140
catcaattgt	cagcggcaga	ttaaatgtgt	ccatatgctt	tgcaattggt	tcaattagta	1200
atgaaatatt	tgaacacaaa	aaaaaaaaa				1229

<210> 61

<211> 1439

<212> DNA

<213> *Lolium perenne*

<400> 61

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gaggatggcg	ccggtggtgg	agagagcgcc	cttcctgccg	acgggggagg	ccacgctgcg	120
gccgtccttc	gtgcgggacg	aggacgagcg	gcccagggtg	gcgcacgacc	gcttcagcga	180
cgaggtgccc	gtcatctcgc	tccacggcat	cgacgacgcg	cggaggaccg	agatccggga	240
ccgcgtggcg	gcgcgtgctg	agggtggggg	catcttccag	gtcgtcgacc	acggcgctcg	300
gcgccgctc	atcgccgaga	tggccaggct	ctcgcgcgac	ttcttcgcgc	tccccgcgca	360
ggcaagctc	cgctacgaca	tgtccggcgg	caagaaggcg	ggattcatcg	tctccagcca	420
cctccagggc	gagacggtcc	aggactggcg	ggagatcgct	acctacttct	cgtaccgggt	480
caaggcgcg	gactacggcc	ggtggccgga	caagcccgcg	gggtggcgcg	cgggtggtgga	540
gcagtacagc	gagcggctca	tggcgtgtgc	ctgcaagctg	ctggggggtg	tgtcggaggc	600
catgggcctg	gagacggagg	ccctgtccaa	ggcgtgcgtg	gacatggacc	agaagggtgg	660
ggtcaacttc	tacccaagt	gccccagcc	cgacctcacc	ctcggcctca	agcgccacac	720
cgaccccgcc	accatcaccc	tcctcctcca	ggacctcgct	ggcggactcc	aggccacccg	780
cgacggcgcc	aacacctgga	tcaccgtaca	gcccacgccc	ggcgcatctg	tcgtcaacct	840
cggcgaccac	ggccactact	tgagcaacgg	gaggtttaag	aacgcggacc	accaggcggt	900
ggtgaacggg	gagagcagca	ggctgtccat	cgccacgttc	cagaaccggg	cgcccgcgcg	960
caaggtgtgg	ccgctggcgg	tgagggaggg	ggaggacacc	atcctggagg	agcccatcac	1020
cttcaccgag	atgtaccgcc	gcaagatggc	gcgcgacctc	gagctcgcca	agcgcaagaa	1080
gcaggccaag	gccgatcagc	tcaagcagca	gctgcagcag	gaggccgcgc	ccgccgcgcg	1140
gccacccaag	ccactcaacc	agattcttgc	ctagattcca	tgccgattca	ttcatgcgtg	1200
atatatagta	ctatgtacta	tatcgtatta	aaataagtaa	ttatctctat	ctactcattt	1260
gtgtgtaatt	aagagatgag	taattatcta	gtatatacac	atctgtctgc	gaggagcgag	1320
ctggacctgt	aataacatgt	agcatgtcct	acgtggaacc	gatcagctga	ttggagctgt	1380
cacatgagtt	tgctgtgtgc	agaaattgaa	cgcattcggt	actgctttca	aaaaaaaaa	1439

<210> 62

<211> 1320

<212> DNA

<213> *Festuca arundinacea*

<400> 62

gaaacggccc	tgactagac	gaaccagaca	aacgactcca	tcccacagac	gactcgccgg	60
ccgccacgcc	cacgcaccac	tttacggggc	cgatcggatc	ggatggcgct	ggtggagaac	120
gcgccgttcc	tgccgacggc	ggcgacgggc	gaggccacgc	tcgggccgct	cttcgtgcgg	180
gacgaggacg	agcgacccaa	ggtggcgcac	gaccgcttca	gcgacgaggt	gccgggtcatc	240
tcgctccacg	gcatcgatga	tggcgggcgc	cggagggccg	agatccggga	ccggtggcgc	300
gcggcgctgc	aagggtgggg	cgtcttccag	gtcgtcgacc	acggcgctcg	cgccgccttc	360
gtcgcggaga	tggccaggct	ctcccgcgag	ttcttcgcac	tccccgcgca	ggacaagctc	420
cgctacgaca	tgtccggcgg	caagaaaggt	ggattcatcg	tctccagcca	cctccagggc	480
gagacggtcc	aggactggcg	ggagatcgct	acctacttct	cgtaccgggt	gaaggcgcg	540
gactacgggc	ggtggccgga	gaagcctgcg	gggtggcgcg	cgtggtgga	gcagtacagc	600
gagcggctca	tggcgctgtc	gtgcaagctg	ctggggggtg	tgtcggaagc	catgggcctg	660
gagacggagg	ccctgtccaa	ggcgtgcgtg	gacatggacc	agaagggtgg	ggtcaacttc	720
tacccaagt	gccccagcc	cgacctcacc	ctcggtctca	agcgccacac	cgaccccggc	780
accatcaccc	tcctcctcca	ggacctcgct	ggcggactcc	aggccactcg	cgacggcgcc	840
aacacctgga	tcaccgtgca	gcccgtcccc	ggcgcccttc	tcgtcaacct	cggcgaccac	900
ggccactact	tgagcaacgg	gaggtttaag	aacgcggacc	accaggcggt	ggtcaacggg	960
gagagcagca	ggctgtccat	cgccacgttc	cagaaccggg	cgccagaagc	gaaggtgtgg	1020
ccgctggcgg	taaggagggg	ggaggacacc	atactggagg	agcccatcac	cttcaccgag	1080
atgtaccgcc	gcaagatggc	gtgcgacctc	gagctcgcca	agcgcaagaa	gcaggccaag	1140

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gccgaccagc tcaagcagca gctgcagcag gagcagcagg aggcgggtggc cgccgccgcg 1200
cccaagcccg ccaccaccaa gccctcaac cagattcttg cctagattcc atgtatatgt 1260
atatcgtatt aaaataagaa attatctata tatatatata tatatataaa aaaaaaaaaa 1320

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<210> 63

<211> 654

<212> PRT

<213> Lolium perenne

<400> 63

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Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Pro Leu Leu Pro
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Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Asp Asp Ala Arg Glu Asn
20     25     30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Val Val Leu Ala
35     40     45
Asp Ser Ala Leu Ala Val Val Val Val Gly Leu Leu Ala Gly Gly
50     55     60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65     70     75     80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85     90     95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100    105    110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115    120    125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130    135    140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145    150    155    160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165    170    175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180    185    190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195    200    205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210    215    220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225    230    235    240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Gly Ile Gly Leu Lys
245    250    255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260    265    270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275    280    285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290    295    300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305    310    315    320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325    330    335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340    345    350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355    360    365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370    375    380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385    390    395    400
Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
405    410    415
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
420    425    430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
435    440    445

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Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
 450 455 460
 Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
 465 470 475 480
 Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
 485 490 495
 Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
 500 505 510
 Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
 515 520 525
 Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
 530 535 540
 Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
 545 550 555 560
 Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
 565 570 575
 Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
 580 585 590
 Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
 595 600 605
 Tyr Pro Thr Glu Thr Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
 610 615 620
 Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
 625 630 635 640
 Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
 645 650

<210> 64

<211> 648

<212> PRT

<213> Festuca arundinacea

<400> 64

Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Arg Leu Leu Pro
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 Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ala Asp Asp Ala Arg Glu Asn
 20 25 30
 Gln Gly Ser Asp Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
 35 40 45
 Ala Ser Ala Leu Ala Val Leu Val Val Val Gly Leu Leu Ala Gly Gly
 50 55 60
 Arg Val Asp Arg Pro Gly Pro Ala Ala Val Pro Ala Val Pro Thr Glu
 65 70 75 80
 Ile Pro Arg Ser Arg Gly Lys Asp Phe Gly Val Ser Glu Lys Ser Ser
 85 90 95
 Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro Trp Ser Asn Ala Met Leu
 100 105 110
 Gln Trp Gln Arg Thr Gly Phe His Phe Gln Pro Glu Gln His Tyr Met
 115 120 125
 Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe
 130 135 140
 Tyr Gln Tyr Asn Pro Lys Gly Asp Ser Trp Gly Asn Ile Ala Trp Ala
 145 150 155 160
 His Ala Val Ser Lys Asp Met Val Asn Trp Arg His Leu Pro Leu Ala
 165 170 175
 Met Val Pro Asp Gln Trp Tyr Asp Ser Asn Gly Val Leu Thr Gly Ser
 180 185 190
 Ile Thr Val Leu Pro Asp Gly Arg Val Ile Leu Leu Tyr Thr Gly Asn
 195 200 205
 Thr Asp Thr Leu Ala Gln Val Gln Cys Leu Ala Glu Pro Ala Asp Pro
 210 215 220
 Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys His Pro Ala Asn Pro Ile
 225 230 235 240
 Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys Asp Phe Arg Asp Pro Leu
 245 250 255
 Thr Asp Trp Phe Asp His Ser Asp Asp Thr Trp Arg Thr Val Ile Gly

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                260                265                270
Ser Lys Asp Asp Gly His Ala Gly Ile Ile Leu Ser Tyr Lys Thr
   275                280                285
Lys Asp Phe Val Asn Tyr Glu Leu Met Pro Gly Asn Met His Arg Gly
   290                295                300
Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile Asp Leu Tyr Pro Val Gly
   305                310                315
Gly Asn Ser Ser Glu Met Leu Gly Gly Asp Asp Ser Pro Asp Val Leu
   325                330                335
Phe Val Leu Lys Glu Ser Ser Asp Asp Glu Arg His Asp Tyr Tyr Ala
   340                345                350
Leu Gly Arg Phe Asp Ala Ala Ala Asn Ile Trp Thr Pro Ile Asp Gln
   355                360                365
Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Tyr Tyr
   370                375                380
Ala Ser Lys Ser Phe Tyr Asp Gln Arg Lys Asn Arg Arg Val Val Trp
   385                390                395
Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln Ala Asp Ile Thr Lys Gly
   405                410                415
Trp Ala Asn Leu Met Thr Ile Pro Arg Thr Val Glu Leu Asp Lys Lys
   420                425                430
Thr Arg Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Val Asp Thr Leu
   435                440                445
Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile Thr Val Asn Ala Gly Ser
   450                455                460
Val Ile Arg Leu Pro Leu His Gln Gly Ala Gln Leu Asp Ile Glu Ala
   465                470                475
Ser Phe Gln Leu Asn Ser Ser Asp Val Asp Ala Leu Asn Glu Ala Asp
   485                490                495
Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala Ala Val Arg Gly Ala Leu
   500                505                510
Gly Pro Phe Gly Leu Leu Val Leu Ala Asn Gly Arg Thr Glu Gln Thr
   515                520                525
Ala Val Tyr Phe Tyr Val Ser Lys Gly Val Asp Gly Ala Leu Gln Thr
   530                535                540
His Phe Cys His Asp Glu Ser Arg Ser Thr Arg Ala Lys Asp Val Val
   545                550                555
Asn Arg Met Ile Gly Ser Ile Val Pro Val Leu Asp Gly Glu Thr Phe
   565                570                575
Ser Val Arg Val Leu Leu Asp His Ser Ile Val Gln Ser Phe Ala Met
   580                585                590
Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala Tyr Pro Thr Glu Ala Ile
   595                600                605
Tyr Ala Ala Ala Gly Val Tyr Val Phe Asn Asn Ala Thr Gly Ala Thr
   610                615                620
Val Thr Ala Glu Arg Leu Val Val Tyr Glu Met Ala Ser Ala Asp Asn
   625                630                635
His Ile Phe Arg Asn Asp Asp Leu
                645

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<210> 65

<211> 620

<212> PRT

<213> Festuca arundinacea

<400> 65

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Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
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Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
  20                25                30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
  35                40                45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
  50                55                60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
  65                70                75                80

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Met	Leu	Gln	Trp	Gln	Arg	Ala	Gly	Phe	His	Tyr	Gln	Pro	Glu	Gly	His
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Phe	Met	Ser	Asp	Pro	Asp	Gly	Pro	Val	Tyr	Tyr	Arg	Gly	Tyr	Tyr	His
			100					105					110		
Leu	Phe	Phe	Gln	Tyr	Asn	Arg	Arg	Gly	Val	Ala	Trp	Asp	Asp	Tyr	Ile
		115					120					125			
Glu	Trp	Gly	His	Val	Val	Ser	Gln	Asp	Leu	Val	His	Trp	Arg	Pro	Leu
	130					135					140				
Pro	Leu	Ala	Leu	Arg	Pro	Asp	His	Trp	Tyr	Asp	Lys	Lys	Gly	Val	Leu
145					150					155					160
Ser	Gly	Thr	Ile	Thr	Val	Leu	His	Asn	Gly	Thr	Leu	Val	Leu	Leu	Tyr
			165						170					175	
Thr	Gly	Val	Thr	Glu	Asp	Pro	Met	Ala	Glu	Ser	Gln	Cys	Ile	Ala	Val
			180					185					190		
Pro	Thr	Asp	Pro	Asn	Asp	Pro	Leu	Leu	Arg	His	Trp	Thr	Lys	His	Pro
		195					200					205			
Ala	Asn	Pro	Val	Leu	Ala	His	Pro	Gln	Gly	Val	Gln	Gly	Met	Asp	Phe
	210					215					220				
Arg	Asp	Pro	Thr	Ser	Ala	Trp	Phe	Asp	Lys	Ser	Asp	Ala	Thr	Trp	Arg
225					230				235						240
Ile	Leu	Ile	Gly	Ser	Lys	Asp	Asp	Asp	Asn	Gly	Ser	His	Ala	Gly	Ile
			245					250						255	
Ala	Phe	Ile	Phe	Lys	Thr	Lys	Asp	Phe	Leu	Ser	Phe	Glu	Arg	Val	Pro
			260					265					270		
Gly	Ile	Val	His	Arg	Val	Glu	Gly	Thr	Gly	Met	Trp	Glu	Cys	Ile	Asp
		275					280					285			
Phe	Tyr	Pro	Val	Gly	Gly	Gly	His	Asn	Ser	Ser	Ser	Glu	Glu	Leu	Tyr
	290					295					300				
Val	Ile	Lys	Ala	Ser	Met	Asp	Asp	Glu	Arg	His	Asp	Tyr	Tyr	Ser	Leu
305					310					315					320
Gly	Arg	Tyr	Asp	Ala	Ala	Ala	Asn	Thr	Trp	Thr	Pro	Leu	Asp	Ala	Glu
			325						330					335	
Leu	Asp	Leu	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Leu	Tyr	Ala
			340					345					350		
Ala	Thr	Ser	Phe	Tyr	Asp	Pro	Leu	Lys	Gln	Arg	Arg	Ile	Met	Leu	Gly
		355					360					365			
Tyr	Val	Gly	Glu	Thr	Asp	Ser	Ala	Arg	Ala	Asp	Val	Ala	Lys	Gly	Trp
	370					375					380				
Ala	Ser	Leu	Gln	Ser	Ile	Pro	Arg	Thr	Val	Thr	Leu	Asp	Glu	Lys	Thr
385					390					395					400
Arg	Thr	Asn	Leu	Leu	Leu	Trp	Pro	Val	Glu	Glu	Val	Glu	Ala	Leu	Arg
			405						410					415	
Tyr	Asn	Ser	Thr	Asp	Leu	Ser	Gly	Ile	Thr	Val	Asp	Asn	Gly	Ser	Val
			420					425					430		
Phe	His	Leu	Pro	Leu	His	Gln	Ala	Thr	His	Leu	Asp	Ile	Glu	Ala	Ser
		435					440					445			
Phe	Arg	Leu	Asp	Ala	Ser	Asp	Val	Ala	Ala	Ile	Asn	Glu	Ala	Asp	Val
	450					455					460				
Gly	Tyr	Asn	Cys	Ser	Ser	Ser	Gly	Gly	Ala	Ala	Ala	Arg	Gly	Ala	Ile
465					470					475					480
Gly	Pro	Phe	Gly	Leu	Leu	Val	His	Ala	Ala	Gly	Asp	Leu	Arg	Gly	Glu
			485						490					495	
Gln	Thr	Ala	Val	Tyr	Phe	Tyr	Val	Ser	Arg	Ala	Leu	Asp	Gly	Thr	Leu
			500					505					510		
Arg	Thr	Ser	Phe	Cys	Asn	Asp	Glu	Thr	Arg	Ser	Ser	Arg	Ala	Arg	Asp
		515					520					525			
Val	Thr	Lys	Arg	Val	Val	Gly	Ser	Thr	Val	Pro	Val	Leu	His	Gly	Glu
	530					535					540				
Ala	Leu	Ser	Met	Arg	Val	Leu	Val	Asp	His	Ser	Ile	Val	Gln	Ser	Phe
545					550					555					560
Ala	Met	Gly	Gly	Arg	Val	Thr	Ala	Thr	Ser	Arg	Val	Tyr	Pro	Thr	Glu
			565						570					575	
Ala	Ile	Tyr	Ala	Arg	Ala	Gly	Val	Tyr	Leu	Phe	Asn	Asn	Ala	Thr	Gly
			580					585					590		
Ala	Ser	Val	Thr	Ala	Glu	Arg	Leu	Ile	Val	His	Glu	Met	Ala	Ser	Ala
		595					600					605			

Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
 610 615 620

<210> 66

<211> 623

<212> PRT

<213> Lolium perenne

<400> 66

Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Gly Ala Thr Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
 65 70 75 80
 Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
 85 90 95
 Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
 100 105 110
 Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
 115 120 125
 Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
 130 135 140
 Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
 145 150 155 160
 Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
 165 170 175
 Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
 180 185 190
 Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
 195 200 205
 Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
 210 215 220
 Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
 225 230 235 240
 Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
 245 250 255
 His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
 260 265 270
 Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
 275 280 285
 Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
 435 440 445

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Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
  450          455          460
Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
465          470          475          480
Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
          485          490          495
Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
          500          505          510
Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
          515          520          525
Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
          530          535          540
Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
545          550          555          560
Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
          565          570          575
Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
          580          585          590
Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
          595          600          605
Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
          610          615          620

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<210> 67

<211> 623

<212> PRT

<213> Festuca arundinacea

<400> 67

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Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
  1          5          10          15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
          20          25          30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
          35          40          45
Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
          50          55          60
Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
65          70          75          80
Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
          85          90          95
Pro Glu Gly His Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg
          100          105          110
Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
          115          120          125
Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
          130          135          140
Trp Arg Pro Leu Pro Val Ala Met Arg Pro Asp His Trp Tyr Asp Lys
145          150          155          160
Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
          165          170          175
Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
          180          185          190
Cys Ile Ala Val Pro Thr Asp Pro Asn Asn Pro Leu Leu Arg His Trp
          195          200          205
Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
          210          215          220
Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp
225          230          235          240
Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
          245          250          255
His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
          260          265          270
Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
          275          280          285

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Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp
 435 440 445
 Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
 450 455 460
 Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
 465 470 475 480
 Arg Gly Ala Ile Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
 485 490 495
 Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
 500 505 510
 Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
 515 520 525
 Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
 530 535 540
 Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
 545 550 555 560
 Val Gln Ser Phe Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val
 565 570 575
 Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
 580 585 590
 Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu
 595 600 605
 Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Gln Asp Ser
 610 615 620

<210> 68

<211> 619

<212> PRT

<213> Lolium perenne

<400> 68

Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
 65 70 75 80
 Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
 85 90 95
 Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
 100 105 110
 Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
 115 120 125

Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
 130 135 140
 Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
 145 150 155 160
 Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
 165 170 175
 Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
 180 185 190
 Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
 195 200 205
 Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ile Phe Glu Arg Val Pro
 260 265 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Asp Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415
 Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Leu
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Glu Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Ala Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
 530 535 540
 Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
 610 615

<210> 69

<211> 422

<212> PRT

<213> Festuca arundinacea

<400> 69

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Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
 1          5          10          15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
          20          25          30
Arg Phe Gly Ala Leu Trp Glu Ser Ala Tyr Cys Gln Asp Ser Leu Leu
          35          40          45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
 50          55          60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
 65          70          75          80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
          85          90          95
Tyr Leu Asn Asn Lys Trp Asp Arg Asn Ile Val Leu Glu Glu Thr Ala
          100          105          110
Lys Tyr Ser Glu Leu Lys Leu Gln Pro Glu Thr Glu Gln Arg Pro His
          115          120          125
Lys Val Ser Phe Leu Val Asp Lys Lys Ser Ala Gln Glu Val Ile Lys
 130          135          140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
 145          150          155          160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
          165          170          175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
          180          185          190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
          195          200          205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
 210          215          220
Glu Glu Leu Leu Gln Trp His Ala Glu Asn Ala Lys Asp Asn Pro Lys
 225          230          235          240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
          245          250          255
Gly His Phe Lys Leu Gly Pro Asn Ile Ser Pro Arg Asp Ile Glu Phe
          260          265          270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
          275          280          285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Ala
 290          295          300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
 305          310          315          320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
          325          330          335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
          340          345          350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
          355          360          365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Ala Trp Val Cys Cys
 370          375          380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
 385          390          395          400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
          405          410          415
Glu Gln Ala Ser Lys Leu
          420

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<210> 70

<211> 422

<212> PRT

<213> Lolium perenne

<400> 70

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Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
 1          5          10          15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
          20          25          30
Arg Phe Gly Ala Leu Trp Glu Ser Thr Tyr Cys Gln Asp Ser Leu Leu
          35          40          45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
          50          55          60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
65          70          75          80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
          85          90          95
Tyr Leu Asn Asn Lys Trp Asp Lys Ser Ile Val Leu Glu Glu Thr Ala
          100          105          110
Lys Phe Ser Glu Leu Lys Leu Gln Ala Glu Thr Glu Gln Arg Pro His
          115          120          125
Lys Val Ser Phe Leu Val Asp Lys Lys Thr Ala Gln Glu Val Ile Lys
130          135          140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
145          150          155          160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
          165          170          175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
          180          185          190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
195          200          205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
210          215          220
Glu Glu Leu Leu Gln Trp Arg Ala Glu Asn Ala Lys Asp Asn Pro Lys
225          230          235          240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
          245          250          255
Gly His Phe Lys Leu Gly Pro Asn Val Ser Pro Arg Asp Val Glu Phe
260          265          270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
275          280          285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Thr
290          295          300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
305          310          315          320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
          325          330          335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
340          345          350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
355          360          365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Lys Trp Val Cys Cys
370          375          380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
385          390          395          400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
          405          410          415
Glu Gln Ala Ser Lys Leu
          420

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<210> 71

<211> 1062

<212> PRT

<213> Festuca arundinacea

<400> 71

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Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
 1          5          10          15
Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
          20          25          30

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Glu	Thr	Ala	Pro	Ala	Leu	Ala	Ala	Glu	Glu	Ser	Gly	Ala	Ala	Tyr	Asn
		35				40						45			
Pro	Thr	Arg	Tyr	Phe	Val	Glu	Glu	Val	Val	Arg	Ser	Phe	Asp	Glu	Gln
	50					55					60				
Ala	Leu	His	Lys	Thr	Trp	Thr	Lys	Val	Val	Ala	Met	Arg	Asn	Ser	Gln
	65				70					75					80
Glu	Arg	Ser	Asn	Arg	Leu	Glu	Asn	Leu	Cys	Trp	Arg	Ile	Trp	Asn	Val
			85						90					95	
Ser	Arg	Gln	Lys	Lys	Gln	Val	Glu	Trp	Asp	Tyr	Thr	Lys	Glu	Val	Ala
			100					105					110		
Arg	Arg	Lys	Leu	Glu	Gln	Glu	Leu	Gly	Ser	Arg	Glu	Ala	Ala	Glu	Asp
		115					120					125			
Leu	Ser	Glu	Leu	Ser	Glu	Gly	Glu	Lys	Asp	Thr	Thr	Ala	Lys	Pro	
	130					135						140			
Asp	Ala	Ala	Thr	Ala	Gln	Pro	Ser	Thr	Asp	Asp	Gly	Glu	His	Gln	Gln
	145				150					155					160
Pro	Gln	Pro	Arg	Thr	Arg	Leu	Ala	Arg	Ile	Asn	Ser	Glu	Val	Arg	Leu
				165					170					175	
Val	Ser	Asp	Asp	Glu	Glu	Glu	Gln	Thr	Lys	Lys	Arg	Asn	Leu	Tyr	Ile
			180					185					190		
Val	Leu	Ile	Ser	Ile	His	Gly	Leu	Val	Arg	Gly	Glu	Asn	Met	Glu	Leu
		195					200					205			
Gly	Arg	Asp	Ser	Asp	Thr	Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Leu
	210					215						220			
Ala	Arg	Ala	Leu	Ala	Ala	Thr	Ala	Gly	Val	His	Arg	Val	Asp	Leu	Leu
	225				230					235					240
Thr	Arg	Gln	Ile	Ser	Cys	Pro	Asp	Val	Asp	Trp	Thr	Tyr	Gly	Glu	Pro
				245					250					255	
Val	Glu	Met	Leu	Glu	Arg	Leu	Ser	Ser	Ala	Asp	Ala	Asp	Glu	Asp	Asp
			260					265					270		
Gly	Glu	Gln	Ser	Gly	Gly	Gly	Ala	Tyr	Ile	Val	Arg	Leu	Pro	Cys	Gly
		275					280					285			
Pro	Arg	Asp	Gln	Tyr	Ile	Pro	Lys	Glu	Glu	Leu	Trp	Pro	His	Ile	Pro
		290				295					300				
Glu	Phe	Val	Asp	Arg	Ala	Leu	Ser	His	Val	Thr	Glu	Val	Ala	Arg	Ala
					310					315					320
Leu	Gly	Asp	Gln	Leu	Gln	Pro	Pro	Pro	Thr	Pro	Ala	Ala	Gly	Asp	Gly
				325					330					335	
Ala	Ala	Leu	Val	Ala	Ala	Pro	Ile	Trp	Pro	Tyr	Val	Ile	His	Gly	His
			340					345					350		
Tyr	Ala	Asp	Ala	Ala	Glu	Val	Ala	Ala	Asn	Leu	Ala	Ser	Ala	Leu	Asn
		355					360					365			
Val	Pro	Met	Val	Met	Thr	Gly	His	Ser	Leu	Gly	Arg	Asn	Lys	Leu	Glu
		370				375					380				
Gln	Leu	Leu	Lys	Leu	Gly	Arg	Met	Pro	Gly	Pro	Glu	Ile	Gln	Gly	Thr
				390						395					400
Tyr	Lys	Ile	Ala	Arg	Arg	Ile	Glu	Ala	Glu	Glu	Thr	Gly	Leu	Asp	Thr
				405					410					415	
Ala	Glu	Met	Val	Val	Thr	Ser	Thr	Lys	Gln	Glu	Ile	Glu	Glu	Gln	Trp
			420					425					430		
Gly	Leu	Tyr	Asp	Gly	Phe	Asp	Leu	Met	Val	Glu	Arg	Lys	Leu	Arg	Val
		435					440					445			
Arg	Gln	Arg	Arg	Gly	Val	Ser	Ser	Leu	Gly	Arg	Tyr	Met	Pro	Arg	Met
		450				455					460				
Ala	Val	Ile	Pro	Pro	Gly	Met	Asp	Phe	Ser	Phe	Val	Glu	Thr	Gln	Asp
					470					475					480
Thr	Ala	Glu	Gly	Asp	Gly	Ala	Asp	Leu	Gln	Met	Leu	Ile	Ala	Pro	Asp
				485					490					495	
Lys	Ala	Lys	Lys	Ala	Leu	Pro	Pro	Ile	Trp	Ser	Asp	Val	Leu	Arg	Phe
			500					505					510		
Phe	Thr	Asn	Pro	His	Lys	Pro	Met	Ile	Leu	Ala	Leu	Ser	Arg	Pro	Asp
		515					520					525			
Pro	Lys	Lys	Asn	Val	Thr	Thr	Leu	Leu	Lys	Ala	Tyr	Gly	Glu	Ser	Arg
		530				535					540				
Gln	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Thr	Leu	Ile	Leu	Gly	Asn	Arg	Asp
					550					555					560

Asp Ile Glu Asp Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val
 565 570 575
 Leu Lys Leu Ile Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro
 580 585 590
 Lys His His Lys Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala
 595 600 605
 Lys Thr Lys Gly Val Phe Thr Asn Pro Ala Leu Val Glu Pro Phe Gly
 610 615 620
 Leu Thr Ile Ile Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr
 625 630 635 640
 Lys Asn Gly Gly Pro Val Asp Ile Leu Lys Ala Leu Asn Asn Gly Leu
 645 650 655
 Leu Val Asp Pro His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser
 660 665 670
 Leu Leu Ala Glu Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu
 675 680 685
 Arg Asn Ile His Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu
 690 695 700
 Ser His Val Ser Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu
 705 710 715 720
 Arg Val Pro Leu Gly Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp
 725 730 735
 Ser Leu Ser Asp Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp
 740 745 750
 Ala Ser Ser Asp Leu Asn Ala Ala Asp Ser Ala Ala Ile Met Asp
 755 760 765
 Ala Leu Arg Arg Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala
 770 775 780
 Arg Ala Leu Gly Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val
 785 790 795 800
 Ala Val Asp Cys Tyr Gly Asp Asp Gly Lys Pro Asp Val Lys Gln Leu
 805 810 815
 Lys Lys Ala Ile Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala
 820 825 830
 Lys Gln Gly Tyr Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala
 835 840 845
 Glu Ala Ile Lys Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu
 850 855 860
 Ile Cys Ser Ser Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Ala
 865 870 875 880
 Ala Asp Glu Glu Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp
 885 890 895
 His Val Lys Ser Ala Val Pro Arg Leu Gly Ser Leu Glu Glu Ile Ala
 900 905 910
 Leu Ala Ile Asp Arg Pro Ala Cys Ser Val His Cys His Ala Tyr Ala
 915 920 925
 Ala Thr Asp Ala Ser Lys Val Lys Lys Val Asp Ser Ile Arg Lys Ser
 930 935 940
 Leu Arg Met Arg Gly Phe Arg Cys Asn Leu Val Tyr Thr Arg Ala Cys
 945 950 955 960
 Thr Arg Leu Asn Val Ile Pro Leu Ser Ala Ser Arg Pro Arg Ala Leu
 965 970 975
 Arg Tyr Leu Ser Ile Gln Trp Gly Ile Asp Leu Ser Lys Val Ala Val
 980 985 990
 Leu Val Gly Glu Thr Gly Asp Thr Asp Arg Glu Arg Leu Leu Pro Gly
 995 1000 1005
 Val His Lys Thr Leu Ile Leu Pro Gly Met Val Ala Arg Gly Ser Glu
 1010 1015 1020
 Glu Leu Leu Arg Gly Asp Asp Gly Tyr Thr Met Ala Asp Val Val Ala
 1025 1030 1035 1040
 Met Asp Ser Pro Asn Ile Val Thr Leu Ala Glu Gly Gln Ser Ala Ser
 1045 1050 1055
 Asp Leu Leu Lys Ala Ile
 1060

<210> 72
 <211> 1074
 <212> PRT
 <213> Lolium perenne

<400> 72

Met	Ala	Gly	Asn	Asp	Trp	Ile	Asn	Ser	Tyr	Leu	Glu	Ala	Ile	Leu	Asp
1				5					10					15	
Ala	Gly	Gly	Thr	Ala	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Val	Ala	Gly	Gly
			20					25					30		
Asp	Asp	Gly	Pro	Gly	Ala	Gly	Gly	Gly	Thr	Ala	Gly	Glu	Lys	Arg	Asp
		35				40						45			
Lys	Ser	Ser	Leu	Met	Leu	Arg	Glu	Arg	Gly	Arg	Phe	Asn	Pro	Ala	Arg
	50					55					60				
Tyr	Phe	Val	Glu	Glu	Val	Ile	Ser	Gly	Phe	Asp	Glu	Thr	Asp	Leu	Tyr
65					70					75				80	
Lys	Thr	Trp	Val	Arg	Thr	Ser	Ala	Met	Arg	Ser	Pro	Gln	Glu	Arg	Asn
				85					90					95	
Thr	Arg	Leu	Glu	Asn	Met	Ser	Trp	Arg	Ile	Trp	Asn	Leu	Ala	Arg	Lys
			100					105					110		
Lys	Lys	Gln	Ile	Glu	Gly	Glu	Glu	Ala	Ser	Arg	Leu	Ser	Lys	Lys	Arg
		115					120					125			
Leu	Glu	Arg	Glu	Lys	Ala	Arg	Arg	Asp	Ala	Ala	Ala	Asp	Leu	Ser	Glu
	130					135					140				
Asp	Leu	Ser	Glu	Gly	Glu	Lys	Gly	Glu	Asn	Ile	Asn	Gly	Ser	Ser	Val
145					150					155				160	
His	Asp	Glu	Ser	Thr	Arg	Gly	Arg	Met	Pro	Arg	Ile	Gly	Ser	Thr	Asp
				165					170					175	
Ala	Ile	Glu	Val	Trp	Ala	Asn	Gln	His	Lys	Asp	Lys	Lys	Leu	Tyr	Ile
			180					185					190		
Val	Leu	Ile	Ser	Ile	His	Gly	Leu	Ile	Arg	Gly	Glu	Asn	Met	Glu	Leu
	195						200					205			
Gly	Arg	Asp	Ser	Asp	Thr	Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Leu
	210					215					220				
Ala	Arg	Ala	Leu	Gly	Glu	Thr	Pro	Gly	Val	Tyr	Arg	Val	Asp	Leu	Leu
225					230					235				240	
Thr	Arg	Gln	Ile	Ser	Ala	Pro	Asp	Val	Asp	Trp	Ser	Tyr	Gly	Glu	Pro
				245					250					255	
Thr	Glu	Met	Leu	Ser	Pro	Arg	Asn	Ser	Glu	Asn	Leu	Gly	Asp	Asp	Met
			260					265					270		
Gly	Glu	Ser	Ser	Gly	Ala	Tyr	Ile	Val	Arg	Ile	Pro	Phe	Gly	Pro	Arg
		275					280					285			
Glu	Lys	Tyr	Ile	Pro	Lys	Glu	Gln	Leu	Trp	Pro	His	Ile	Gln	Glu	Phe
	290					295					300				
Val	Asp	Gly	Ala	Leu	Val	His	Ile	Met	Gln	Met	Ser	Lys	Val	Leu	Gly
305					310					315				320	
Glu	Gln	Val	Gly	Arg	Glu	Arg	Arg	Val	Trp	Pro	Val	Val	Ile	His	Gly
				325					330					335	
His	Tyr	Ala	Asp	Ala	Gly	Asp	Ser	Ala	Ala	Leu	Leu	Ser	Gly	Ala	Leu
			340					345					350		
Asn	Val	Pro	Met	Val	Phe	Thr	Gly	His	Ser	Leu	Gly	Arg	Asp	Lys	Leu
		355					360					365			
Glu	Gln	Leu	Leu	Lys	Gln	Gly	Arg	Gln	Thr	Arg	Asp	Glu	Val	Asn	Ala
	370					375					380				
Thr	Tyr	Lys	Ile	Met	Arg	Arg	Ile	Glu	Ala	Glu	Glu	Leu	Cys	Leu	Asp
385					390					395				400	
Ala	Ser	Glu	Ile	Val	Ile	Thr	Ser	Thr	Arg	Gln	Glu	Ile	Glu	Lys	Gln
				405					410					415	
Trp	Gly	Leu	Tyr	Asn	Gly	Phe	Asp	Val	Thr	Met	Glu	Arg	Lys	Leu	Arg
			420					425					430		
Ala	Arg	Thr	Lys	Arg	Gly	Val	Ser	Cys	Tyr	Gly	Arg	Tyr	Met	Pro	Arg
			435				440					445			
Met	Ile	Ala	Ile	Pro	Pro	Gly	Met	Glu	Phe	Ser	His	Ile	Val	Pro	His
						455					460				
Asp	Val	Asp	Leu	Asp	Gly	Asp	Glu	Ala	Asn	Glu	Val	Gly	Ser	Gly	Ser
465					470					475				480	

Pro	Asp	Pro	Pro	Ile	Trp	Ala	Asp	Ile	Met	Arg	Phe	Phe	Ser	Asn	Pro		
				485					490					495			
Arg	Lys	Pro	Met	Ile	Leu	Ala	Leu	Ala	Arg	Pro	Asp	Pro	Lys	Lys	Asn		
			500					505					510				
Ile	Thr	Thr	Leu	Val	Lys	Ala	Phe	Gly	Glu	His	Pro	Gly	Leu	Arg	Asn		
		515					520					525					
Leu	Ala	Asn	Leu	Thr	Leu	Ile	Met	Gly	Asn	Arg	Asp	Val	Ile	Asp	Glu		
		530				535					540						
Met	Ser	Ser	Thr	Asn	Gly	Ala	Val	Leu	Thr	Ser	Val	Leu	Lys	Leu	Ile		
545					550					555					560		
Asp	Lys	Tyr	Asp	Leu	Tyr	Gly	Gln	Val	Ala	Tyr	Pro	Lys	His	His	Lys		
				565					570					575			
Gln	Ser	Glu	Val	Pro	Asp	Ile	Tyr	Arg	Leu	Ala	Ala	Arg	Thr	Lys	Gly		
			580					585					590				
Val	Phe	Ile	Asn	Cys	Ala	Tyr	Ile	Glu	Pro	Phe	Gly	Leu	Thr	Leu	Ile		
		595					600					605					
Glu	Ala	Ala	Ala	Tyr	Gly	Leu	Pro	Met	Val	Ala	Thr	Gln	Asn	Gly	Gly		
		610				615					620						
Pro	Val	Asp	Ile	His	Arg	Val	Leu	Asp	Asn	Gly	Ile	Leu	Val	Asp	Pro		
625					630					635					640		
His	Asn	Gln	Asn	Asp	Ile	Ala	Glu	Ala	Leu	Tyr	Lys	Leu	Val	Ser	Asp		
				645					650					655			
Lys	His	Leu	Trp	Ala	Gln	Cys	Arg	Gln	Asn	Gly	Leu	Asp	Asn	Ile	His		
			660					665					670				
Arg	Phe	Ser	Trp	Pro	Glu	His	Cys	Lys	Asn	Tyr	Leu	Ser	Arg	Val	Gly		
		675					680					685					
Thr	Val	Lys	Pro	Arg	His	Pro	Arg	Trp	Gln	Arg	Ser	Asp	Asp	Ala	Thr		
		690				695					700						
Glu	Val	Ser	Glu	Ser	Asp	Ser	Pro	Gly	Asp	Ser	Leu	Arg	Asp	Val	His		
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Asp	Ile	Ser	Leu	Asn	Leu	Lys	Leu	Ser	Leu	Asp	Ser	Glu	Lys	Ala	Gly		
				725					730					735			
Thr	Lys	Ile	Asn	Thr	Glu	Arg	Asn	Ser	Thr	Asn	Ala	Arg	Arg	Asn	Leu		
			740					745					750				
Glu	Asp	Ala	Val	Leu	Lys	Phe	Ser	Asn	Ala	Val	Ser	Glu	Gly	Thr	Lys		
		755					760					765					
Asp	Glu	Ser	Asp	Glu	Asn	Ala	Glu	Ala	Thr	Thr	Gly	Ser	Ile	Asn	Gly		
		770				775					780						
His	Leu	Tyr	Gly	Glu	Lys	His	Ile	Val	Val	Ile	Ala	Val	Asp	Ser	Val		
785					790					795					800		
Gln	Asn	Ala	Asp	Leu	Val	Gln	Ile	Ile	Lys	Asn	Leu	Phe	Glu	Ala	Ser		
				805					810					815			
Arg	Lys	Glu	Lys	Ser	Ser	Gly	Ala	Val	Gly	Phe	Val	Leu	Ser	Thr	Ser		
			820						825					830			
Arg	Ala	Ile	Ser	Glu	Thr	Leu	Thr	Phe	Leu	Thr	Ser	Gly	Gly	Ile	Gln		
		835					840						845				
Thr	Thr	Glu	Phe	Asp	Ala	Phe	Ile	Cys	Ser	Ser	Gly	Ser	Asp	Leu	Cys		
		850				855					860						
Tyr	Pro	Ser	Ser	Ser	Ser	Glu	Asp	Met	Leu	Ser	Pro	Thr	Glu	Leu	Pro		
865					870					875					880		
Phe	Met	Ile	Asp	Leu	Asp	Tyr	His	Ser	Gln	Ile	Glu	Tyr	Arg	Trp	Gly		
				885					890					895			
Gly	Glu	Gly	Leu	Arg	Lys	Thr	Leu	Ile	Arg	Trp	Ala	Ala	Glu	Asn	Asn		
			900					905					910				
Ser	Gln	Ser	Gly	Gln	Glu	Val	Val	Thr	Glu	Asp	Glu	Glu	Cys	Ser	Ser		
		915						920				925					
Thr	Tyr	Cys	Ile	Ser	Phe	Lys	Val	Lys	Asn	Thr	Glu	Ala	Val	Pro	Pro		
		930				935					940						
Val	Lys	Asp	Leu	Arg	Lys	Thr	Met	Arg	Ile	Gln	Ala	Leu	Arg	Cys	His		
945					950					955					960		
Val	Leu	Tyr	Ser	His	Asp	Gly	Ser	Lys	Leu	Asn	Leu	Ile	Pro	Leu	Leu		
				965					970					975			
Ala	Ser	Arg	Ser	Gln	Ala	Leu	Arg	Tyr	Leu	Tyr	Ile	Arg	Trp	Gly	Val		
			980					985					990				
Glu	Leu	Ala	Asn	Met	Thr	Val	Val	Val	Gly	Glu	Ser	Gly	Asp	Thr	Asp		
			995					1000					1005				

Tyr Glu Gly Leu Leu Gly Gly Val His Lys Thr Ile Ile Leu Lys Gly
 1010 1015 1020
 Ser Phe Asn Ala Ala Pro Asn Gln Leu His Ala Ala Arg Ser Tyr Ser
 1025 1030 1035 1040
 Leu Glu Asp Val Ile Ser Phe Asp Lys Pro Gly Ile Ala Ser Val Glu
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 Gly Tyr Leu Pro Asp Ser Leu Lys Ser Ala Leu Gln Gln Phe Gly Val
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 Leu Asn

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 Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Ser Ala Ala Tyr Asn
 35 40 45
 Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
 50 55 60
 Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
 65 70 75 80
 Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
 85 90 95
 Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
 100 105 110
 Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
 115 120 125
 Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Thr Ala Lys Pro
 130 135 140
 Asp Ala Ala Ala Ala Gln Pro Ser Ala Asp Asp Gly Glu His Gln Gln
 145 150 155 160
 Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
 165 170 175
 Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
 245 250 255
 Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp
 260 265 270
 Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
 275 280 285
 Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
 290 295 300
 Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
 305 310 315 320
 Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
 325 330 335
 Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
 340 345 350
 Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
 355 360 365
 Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
 370 375 380

Leu	Gly	Arg	Met	Pro	Gly	Pro	Glu	Ile	Gln	Gly	Thr	Tyr	Lys	Ile	Ala
385					390					395					400
Arg	Arg	Ile	Glu	Ala	Glu	Glu	Thr	Gly	Leu	Asp	Thr	Ala	Glu	Met	Val
				405					410					415	
Val	Thr	Ser	Thr	Lys	Gln	Glu	Ile	Glu	Glu	Gln	Trp	Gly	Leu	Tyr	Asp
			420					425					430		
Gly	Phe	Asp	Leu	Met	Val	Glu	Arg	Lys	Leu	Arg	Val	Arg	Gln	Arg	Arg
		435					440					445			
Gly	Val	Ser	Ser	Leu	Gly	Arg	Tyr	Met	Pro	Arg	Met	Ala	Val	Ile	Pro
	450					455					460				
Pro	Gly	Met	Asp	Phe	Ser	Phe	Val	Glu	Thr	Gln	Asp	Thr	Ala	Asp	Gly
465					470					475					480
Thr	Gly	Arg	Ser	Gln	Met	Leu	Ile	Ala	Pro	Asp	Lys	Ala	Lys	Lys	Ala
				485					490					495	
Leu	Pro	Pro	Ile	Trp	Ser	Asp	Val	Leu	Arg	Phe	Phe	Thr	Asn	Pro	His
			500					505					510		
Lys	Pro	Met	Ile	Leu	Ala	Leu	Ser	Arg	Pro	Asp	Pro	Lys	Lys	Asn	Val
		515					520					525			
Thr	Thr	Leu	Leu	Lys	Ala	Tyr	Gly	Glu	Ser	Arg	Gln	Leu	Arg	Glu	Leu
	530					535					540				
Ala	Asn	Leu	Thr	Leu	Ile	Leu	Gly	Asn	Arg	Asp	Asp	Ile	Glu	Asp	Met
545					550					555					560
Ala	Gly	Gly	Gly	Gly	Ala	Val	Leu	Thr	Ala	Val	Leu	Lys	Leu	Ile	Asp
				565					570					575	
Arg	Tyr	Asp	Leu	Tyr	Gly	Gln	Val	Ala	Tyr	Pro	Lys	His	His	Lys	Gln
			580					585					590		
Thr	Asp	Val	Pro	His	Ile	Tyr	Arg	Leu	Ala	Ala	Lys	Thr	Lys	Gly	Val
		595					600					605			
Phe	Ile	Asn	Pro	Ala	Leu	Val	Glu	Pro	Phe	Gly	Leu	Thr	Ile	Ile	Glu
	610					615					620				
Ala	Ala	Ala	Tyr	Gly	Leu	Pro	Val	Val	Ala	Thr	Lys	Asn	Gly	Gly	Pro
625					630					635					640
Val	Asp	Ile	Leu	Lys	Ala	Leu	His	Asn	Gly	Leu	Leu	Val	Asp	Pro	His
				645					650					655	
Ser	Ala	Glu	Ala	Ile	Thr	Gly	Ala	Leu	Leu	Ser	Leu	Leu	Ala	Glu	Lys
			660					665					670		
Ser	Arg	Trp	Val	Glu	Cys	Arg	Arg	Asn	Gly	Leu	Arg	Asn	Ile	His	Arg
		675					680					685			
Phe	Ser	Trp	Pro	His	His	Cys	Arg	Leu	Tyr	Leu	Ser	His	Val	Ser	Thr
	690					695				700					
Tyr	Cys	Asp	Gln	Pro	Ser	Pro	His	Gln	Pro	Leu	Arg	Val	Pro	Leu	Ala
705					710					715					720
Leu	Gly	Ser	Ser	Thr	Ser	Phe	Gly	Ala	Asp	Asp	Ser	Leu	Ser	Asp	Ser
				725					730					735	
Leu	Arg	Gly	Leu	Ser	Leu	Gln	Ile	Ser	Val	Asp	Ala	Ser	Ser	Asp	Leu
			740					745					750		
Asn	Ala	Ala	Asp	Ser	Ala	Ala	Ala	Ile	Met	Asp	Ala	Leu	Arg	Arg	Arg
		755					760					765			
Pro	Ala	Ser	Glu	Lys	Pro	Ala	Ser	Ser	Gly	Ala	Arg	Ala	Leu	Gly	Phe
	770					775					780				
Ala	Pro	Gly	Arg	Arg	Glu	Ser	Leu	Leu	Val	Val	Ala	Val	Asp	Cys	Tyr
785					790					795					800
Gly	Asp	Asp	Gly	Lys	Pro	Asp	Val	Glu	Gln	Leu	Lys	Lys	Ala	Ile	Asp
				805					810					815	
Ala	Ala	Val	Ser	Val	Gly	Glu	Cys	Ala	Gly	Ala	Lys	Gln	Gly	Tyr	Val
			820					825					830		
Leu	Ser	Thr	Gly	Met	Thr	Ile	Pro	Glu	Ala	Ala	Glu	Ala	Ile	Lys	Ala
		835					840					845			
Cys	Gly	Ala	Asp	Val	Ala	Ser	Phe	Asp	Ala	Leu	Ile	Cys	Ser	Ser	Gly
	850					855					860				
Ala	Glu	Leu	Cys	Tyr	Pro	Trp	Lys	Lys	Leu	Val	Ala	Asp	Glu	Glu	Tyr
865					870					875					880
Ser	Gly	His	Val	Ala	Phe	Arg	Trp	Pro	Gly	Asp	His	Val	Lys	Ser	Ala
				885					890					895	
Val	Pro	Arg	Leu	Gly	Ser	Met	Glu	Glu	Ile	Ala	Leu	Ala	Ile	Asp	Arg
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Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala Ser
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 Lys Val Ser Ile Thr Glu His Tyr Leu
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 20 25 30
 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
 35 40 45
 Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
 50 55 60
 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
 65 70 75 80
 Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
 85 90 95
 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
 100 105 110
 Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
 115 120 125
 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
 130 135 140
 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
 145 150 155 160
 Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
 165 170 175
 Asn Phe Leu Lys Ala His Asn His Gln Gly Thr Thr Met Met Leu Asn
 180 185 190
 Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
 195 200 205
 Glu Glu Tyr Leu Thr Ser Ile Pro Glu Asp Thr Pro Ser Ser Glu Phe
 210 215 220
 Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
 225 230 235 240
 Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Asp Leu Leu Glu
 245 250 255
 Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
 260 265 270
 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
 275 280 285
 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
 290 295 300
 Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
 305 310 315 320
 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
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 Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
 340 345 350
 Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
 355 360 365
 Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
 370 375 380
 Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
 385 390 395 400
 Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
 405 410 415
 Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
 420 425 430

His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
 435 440 445
 Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
 450 455 460
 Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
 465 470 475 480
 Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
 485 490 495
 Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
 500 505 510
 Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Thr Val Tyr
 515 520 525
 Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
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 Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
 545 550 555 560
 Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
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 Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
 580 585 590
 Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
 595 600 605
 Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
 610 615 620
 Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Glu Gly His Ile Arg Trp Ile
 625 630 635 640
 Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
 645 650 655
 Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
 660 665 670
 Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
 675 680 685
 Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asn Gly Val Ser Gly
 690 695 700
 Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
 705 710 715 720
 Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
 725 730 735
 Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
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 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Val Pro Leu Ala
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 Val Asp Gly Glu Asn Thr Asp Asn
 805

<210> 75

<211> 808

<212> PRT

<213> Festuca arundinacea

<400> 75

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 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
 35 40 45
 Glu Phe Glu Ala Leu Phe Glu Ser Asp Lys Glu Arg Tyr Ala Pro Phe
 50 55 60
 Gln Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
 65 70 75 80

Val	Ala	Leu	Ala	Ile	Arg	Pro	Arg	Pro	Gly	Val	Trp	Asp	Tyr	Ile	Arg
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Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Thr	Val	Ser	Glu	Tyr
			100					105					110		
Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Glu	His	Ala	Ser	Ser	Lys	Phe
		115					120					125			
Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe	Pro	Arg	Pro
	130					135					140				
Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	Asn	Arg	His
145					150					155				160	
Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr	Pro	Leu	Leu
				165					170					175	
Asn	Phe	Leu	Lys	Ala	His	Asn	His	Lys	Gly	Thr	Thr	Met	Met	Leu	Asn
			180					185					190		
Asp	Arg	Ile	Thr	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ala	Leu	Arg	Lys	Ala
		195					200					205			
Glu	Glu	Tyr	Leu	Thr	Ser	Ile	Leu	Glu	Asp	Thr	Pro	Ser	Phe	Glu	Phe
	210					215					220				
Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr
225					230					235				240	
Ala	Lys	Arg	Val	Gln	Asp	Thr	Ile	His	Leu	Leu	Leu	Asp	Leu	Leu	Glu
				245					250					255	
Ala	Pro	Asp	Pro	Ala	Ser	Leu	Glu	Lys	Phe	Leu	Gly	Thr	Ile	Pro	Met
			260					265					270		
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Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val	Tyr	Ile	Leu
	290					295					300				
Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg	Ile	Lys	Gln
305					310					315				320	
Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr	Arg	Leu	Leu
				325					330					335	
Pro	Asp	Ala	Val	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
			340					345					350		
Gly	Thr	Glu	His	Thr	Asp	Ile	Leu	Arg	Val	Pro	Phe	Arg	Thr	Glu	Lys
		355					360					365			
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
	370					375					380				
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ala	Asn	Glu	Leu	Met	Arg	Glu	Met	Gln
385					390					395				400	
Thr	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
				405					410					415	
Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala
				420				425					430		
His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asn	Ser	Asp	Ile	Tyr	Leu	Asp
		435					440					445			
Lys	Phe	Asp	Ser	Gln	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr	Ala	Asp	Leu
	450						455				460				
Ile	Ala	Met	Asn	His	Thr	Asp	Phe	Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu
465					470					475				480	
Ile	Ala	Gly	Ser	Lys	Asp	Ser	Val	Gly	Gln	Tyr	Glu	Ser	His	Ile	Ala
				485					490					495	
Phe	Thr	Leu	Pro	Asp	Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe
			500					505					510		
Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Ser	Val	Tyr
		515					520					525			
Phe	Pro	Tyr	Thr	Glu	Thr	Asp	Lys	Arg	Leu	Thr	Ala	Phe	His	Pro	Glu
	530					535					540				
Ile	Glu	Glu	Leu	Leu	Tyr	Ser	Asp	Val	Glu	Asn	Ser	Glu	His	Lys	Phe
545					550					555				560	
Val	Leu	Lys	Asp	Lys	Asn	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu
				565					570					575	
Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Phe	Gly	Lys	Asn
			580					585					590		
Ala	His	Leu	Lys	Asp	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala	Gly	Asp	His
		595					600						605		

Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
 610 615 620
 Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Lys Gly His Ile Arg Trp Ile
 625 630 635 640
 Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
 645 650 655
 Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
 660 665 670
 Gly Leu Thr Val Ile Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
 675 680 685
 Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asp Gly Val Ser Gly
 690 695 700
 Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
 705 710 715 720
 Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
 725 730 735
 Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
 770 775 780
 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Val Pro Leu Ala
 785 790 795 800
 Val Asp Gly Glu Asn Thr Asp Ser
 805

<210> 76

<211> 814

<212> PRT

<213> Lolium perenne

<400> 76

Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
 20 25 30
 Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
 130 135 140
 Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
 145 150 155 160
 Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
 165 170 175
 Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
 180 185 190
 Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
 195 200 205
 Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
 210 215 220
 Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
 225 230 235 240
 Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
 245 250 255

Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
 260 265 270
 Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
 275 280 285
 His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
 290 295 300
 Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
 305 310 315 320
 Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
 325 330 335
 Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
 340 345 350
 Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
 355 360 365
 Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
 370 375 380
 Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His
 385 390 395 400
 Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
 405 410 415
 Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
 420 425 430
 Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
 435 440 445
 Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
 450 455 460
 Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
 465 470 475 480
 Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
 485 490 495
 Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
 500 505 510
 Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
 515 520 525
 Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
 530 535 540
 Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Tyr Ser Asp Val
 545 550 555 560
 Asp Asn Asp Glu His Ser Cys Leu Lys Asp Arg Asn Lys Pro Ile Ile
 565 570 575
 Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val
 580 585 590
 Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu Val
 595 600 605
 Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu Gln
 610 615 620
 Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu Asn
 625 630 635 640
 Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn Ala
 645 650 655
 Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro
 660 665 670
 Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr Cys
 675 680 685
 Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile Ile
 690 695 700
 Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp Lys
 705 710 715 720
 Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp His
 725 730 735
 Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu Glu
 740 745 750
 Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly
 755 760 765
 Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr
 770 775 780

Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met Ala
 785 790 795 800
 Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
 805 810

<210> 77
 <211> 816
 <212> PRT
 <213> Festuca arundinacea

<400> 77
 Met Gly Glu Ser Ala Gly Glu Arg Ala Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Thr Asn Glu Leu Val
 20 25 30
 Ala Val Phe Ser Arg Leu Val Asn His Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Thr Ala Glu Tyr Asn Ala Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Thr Ala Phe Glu Asp Leu Leu Arg Gly Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Gly Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Asn Glu Ser Thr Asp Asn Asn Phe Val Leu Glu Leu Asp Phe Gly Pro
 130 135 140
 Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn
 145 150 155 160
 Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp
 165 170 175
 Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
 180 185 190
 Lys Gly Met Thr Met Met Leu Asn Asp Arg Ile Arg Ser Leu Ser Ala
 195 200 205
 Leu Gln Asp Ala Leu Arg Lys Ala Glu Lys His Leu Ser Gly Leu Pro
 210 215 220
 Ala Asp Thr Pro Tyr Ser Glu Phe His His Arg Phe Gln Glu Leu Gly
 225 230 235 240
 Leu Glu Lys Gly Trp Gly Asp Cys Thr Gln Arg Ala His Glu Thr Ile
 245 250 255
 His Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu
 260 265 270
 Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser
 275 280 285
 Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr
 290 295 300
 Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn
 305 310 315 320
 Glu Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Lys
 325 330 335
 Ile Leu Ile Val Thr Arg Leu Leu Pro Asp Ala His Gly Thr Thr Cys
 340 345 350
 Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu
 355 360 365
 Arg Val Pro Phe Lys Thr Glu Asp Gly Ile Val Arg Lys Trp Ile Ser
 370 375 380
 Arg Phe Glu Val Trp Pro Tyr Leu Glu Ala Tyr Thr Asp Asp Val Ala
 385 390 395 400
 His Glu Ile Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly
 405 410 415
 Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Leu
 420 425 430

Gly Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr
 435 440 445
 Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe
 450 455 460
 Ser Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Ala Asp Phe
 465 470 475 480
 Ile Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val
 485 490 495
 Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
 500 505 510
 Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
 515 520 525
 Pro Gly Ala Asp Met Thr Ile Tyr Phe Pro Tyr Thr Glu Gln Gln Lys
 530 535 540
 Arg Leu Thr Ser Leu His Ala Glu Ile Glu Glu Leu Leu Phe Ser Asp
 545 550 555 560
 Val Glu Asn Ser Glu His Lys Phe Val Leu Lys Asp Lys Asn Lys Pro
 565 570 575
 Ile Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly
 580 585 590
 Leu Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn
 595 600 605
 Leu Val Val Val Cys Gly Asp His Gly Lys Glu Ser Lys Asp Lys Glu
 610 615 620
 Glu Gln Ala Glu Phe Lys Arg Met Phe Asp Leu Ile Glu Gln Tyr Asn
 625 630 635 640
 Leu Ser Ser His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg
 645 650 655
 Asn Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Met Lys Gly Ala Phe Val
 660 665 670
 Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met
 675 680 685
 Thr Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu
 690 695 700
 Ile Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Asn
 705 710 715 720
 Asp Lys Ala Ser Ala Leu Leu Val Glu Phe Glu Lys Cys Gln Glu
 725 730 735
 Asp Pro Ser His Trp Asn Lys Ile Ser Gln Gly Gly Leu Gln Arg Ile
 740 745 750
 Glu Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu
 755 760 765
 Ser Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Asp Arg Arg
 770 775 780
 Glu Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Lys
 785 790 795 800
 Met Ala Thr Thr Val Pro Leu Ala Ile Glu Gly Glu Thr Thr Gly Lys
 805 810 815

<210> 78

<211> 478

<212> PRT

<213> Festuca arundinacea

<400> 78

Trp Ile Ile Leu Glu Pro Ala Ile Glu Pro Asp Thr Pro Gly Asp Ile
 1 5 10 15
 Lys Gly Cys Trp Ser Ala Ser Ala Thr Val Ile Ser Gly Ser Gln Pro
 20 25 30
 Val Ile Met Tyr Thr Gly Gly Asp Val Glu Asn His Gln Val Gln Asn
 35 40 45
 Ile Ala Leu Pro Lys Asn Arg Ser Asp Pro Tyr Leu Ile Glu Trp Thr
 50 55 60
 Lys Ala Cys Asn Asn Pro Val Leu Gln Pro Val Gly Pro Gly Met Asn
 65 70 75 80

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Pro Gly Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro Asp Gly
      85      90      95
Leu Trp Arg Ile Ser Ile Gly Ala Glu Val Asn Gly Tyr Ser Ala Ala
      100      105      110
Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Ser Arg Val Asp His
      115      120      125
Pro Leu Tyr Ser Ser Ser Ala Ser Thr Met Trp Glu Cys Leu Asp Phe
      130      135      140
Phe Ala Val Leu Pro Gly Ser Asn Gly Gly Leu Asp Leu Ser Ala Ala
      145      150      155      160
Ile Pro Lys Gly Ala Lys His Val Leu Lys Val Ser Val Asp Gln Cys
      165      170      175
Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Glu His Asp Ala Phe Val
      180      185      190
Pro Asp Thr Ile Leu Asp Asp Arg Trp Leu Leu Pro Arg Ile Asp Tyr
      195      200      205
Gly Asn Tyr Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Asn Arg Arg
      210      215      220
Arg Ile Ile Trp Gly Trp Thr Asn Glu Ser Asp Ser Ser Ser Asp Asp
      225      230      235      240
Val Ala Lys Gly Trp Ala Gly Ile Tyr Ala Ile Pro Arg Thr Ile Trp
      245      250      255
Leu Asp Arg Asp Gly Lys Gln Leu Leu Gln Trp Pro Val Glu Glu Ile
      260      265      270
Glu Ser Leu Arg Arg Asn Glu Ile Asn Tyr Gln Gly Leu Asp Leu Glu
      275      280      285
Lys Gly Asp Leu Tyr Glu Ile Lys Gly Val Asp Thr Leu Gln Ala Asp
      290      295      300
Val Glu Ile Asp Phe Glu Leu Thr Ser Ile Asp Asp Ala Asp Ser Phe
      305      310      315      320
Asp Pro Ser Trp Leu Leu Asp Pro Glu Lys His Cys Arg Glu Ala Gly
      325      330      335
Ala Ser Val His Gly Gly Ile Gly Pro Phe Gly Leu Val Ile Leu Ala
      340      345      350
Thr Gly Asp Met Glu Glu His Thr Val Val His Phe Arg Val Tyr Lys
      355      360      365
Ser Gln Lys Glu Tyr Met Ile Leu Met Cys Ser Asp Ile Arg Arg Ser
      370      375      380
Ser Leu Arg Gln Gly Leu Tyr Ala Pro Ala Tyr Gly Gly Phe Phe Glu
      385      390      395      400
Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp
      405      410      415
Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys Ile Ile
      420      425      430
Ala Arg Val Tyr Pro Val Ala Ile Val Asp Asp Gly Ser Ala His Met
      435      440      445
Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Ile Arg
      450      455      460
Ala Trp Ser Met Met Thr Ala Gln Val Asn Leu Lys Lys Gly
      465      470      475

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<210> 79

<211> 583

<212> PRT

<213> Lolium perenne

<400> 79

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Met Gly Asn Pro Lys Trp Val Leu Ala Pro Trp Ala Val Leu Leu Leu
  1      5      10      15
Leu Gln Leu Ala Ser Ala Ser His His Ala Arg Leu Ser Leu Glu Thr
      20      25      30
Ser Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro Leu Leu
      35      40      45
Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn Asp Pro
      50      55      60

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Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr
 65 70 75 80
 Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His Ser Val
 85 90 95
 Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile Ser Pro
 100 105 110
 Thr Ile Pro Thr Asp Gln Tyr Gly Val Trp Ser Gly Ser Thr Thr Ile
 115 120 125
 Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp Arg Pro
 130 135 140
 Ser Val Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn Ala Ser
 145 150 155 160
 Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro Ile Ala
 165 170 175
 Val Pro Val Glu Gly Ile Asn Ala Thr Gln Phe Arg Asp Pro Thr Thr
 180 185 190
 Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly Leu Arg
 195 200 205
 Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Arg Asp Phe
 210 215 220
 Lys His Trp Val Arg Ala Lys His Pro Leu His Ser Ala Leu Thr Gly
 225 230 235 240
 Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Lys Ala Gly Val Glu
 245 250 255
 Lys Gly Leu Asp Thr Ser Glu Tyr Gly Ala Ala Ala Gly Val Glu Lys
 260 265 270
 His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
 275 280 285
 Ile Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
 290 295 300
 Thr Gly Asp Val Tyr Gln Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
 305 310 315 320
 Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
 325 330 335
 Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
 340 345 350
 Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
 355 360 365
 Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
 370 375 380
 Gly Lys Pro Val Asn Val Gly Asp Lys Val Val Lys Pro Gly Gln His
 385 390 395 400
 Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
 405 410 415
 Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
 420 425 430
 Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Val Lys
 435 440 445
 Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ser Ser Ala Asp Leu
 450 455 460
 Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
 465 470 475 480
 Lys Pro Ile Val Leu Met Cys Ser Asp Pro Thr Lys Ser Ser Leu Thr
 485 490 495
 Pro Asp Leu Tyr Lys Pro Thr Phe Ala Gly Phe Val Asp Thr Asp Ile
 500 505 510
 Ser Ser Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp Arg Ser Val Val
 515 520 525
 Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Leu Ser Arg Val Tyr
 530 535 540
 Pro Ser Met Ala Leu Gly Lys Asp Ala His Leu His Val Phe Asn Asn
 545 550 555 560
 Gly Glu Thr Asp Ile Lys Val Ser Lys Leu Thr Ala Trp Glu Met Lys
 565 570 575
 Arg Pro Leu Met Asn Gly Ala
 580

<210> 80
 <211> 390
 <212> PRT
 <213> Lolium perenne

<400> 80
 Gly Val Gly Ser Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp
 1 5 10 15
 Gln Arg Asn Ala Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val
 20 25 30
 Leu Glu Cys Pro Asp Leu Phe Pro Val Ala Ala Ala Gln Gly Ala
 35 40 45
 Thr Glu Gly Leu Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His
 50 55 60
 Val Leu Lys Leu Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly
 65 70 75 80
 Phe Tyr Asp Asp Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg
 85 90 95
 Gly Asp Asp Pro Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr
 100 105 110
 Ala Ser Lys Ser Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp
 115 120 125
 Ala Trp Val Asp Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala
 130 135 140
 Gly Ile Gln Ala Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys
 145 150 155 160
 Arg Leu Val Gln Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys
 165 170 175
 Arg Val Gly Leu Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys
 180 185 190
 Glu Ile Ala Gly Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe
 195 200 205
 Glu Ile Pro Asn Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val
 210 215 220
 Leu Asp Pro Lys Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly
 225 230 235 240
 Gly Val Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu
 245 250 255
 Glu His Thr Ala Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr
 260 265 270
 Lys Val Leu Met Cys Thr Asp Leu Thr Lys Ser Ser Thr Lys Ala Gly
 275 280 285
 Ala His Lys Pro Ser Tyr Gly Ala Phe Leu Asp Val Asp Val Glu Lys
 290 295 300
 Asp Lys Phe Ile Ser Leu Arg Thr Leu Ile Asp His Thr Val Val Glu
 305 310 315 320
 Ser Phe Gly Asp Gly Gly Arg Thr Cys Met Thr Ala Arg Val Tyr Pro
 325 330 335
 Glu His Ala Ala Met Gly Ser Thr His Leu Tyr Val Phe Asn Asn Gly
 340 345 350
 Thr Gly Ala Val Lys Val Ser Lys Leu Glu Ala Trp Glu Leu Ala Thr
 355 360 365
 Ala Ala Val Asn Gly Gly Ser Leu Ala Pro Val Val Val Lys Ala Ser
 370 375 380
 Asp Pro Lys Glu Ala Leu
 385 390

<210> 81
 <211> 597
 <212> PRT
 <213> Festuca arundinacea

<400> 81
 Met Ala Gly Leu Arg Leu Ala Ala Cys Ala Ala Val Ala Val Leu Leu
 1 5 10 15

Cys Leu Leu Leu Ser Ser Ser Ala Ala Leu Arg Trp Leu Ser Asp Pro
 20 25 30
 Ala Pro Glu Ser Ala Ala Ala Gly Val Ser His Asp Ser Tyr Arg Thr
 35 40 45
 Ala Tyr His Phe Gln Pro Thr Glu Asn Trp Gln Asn Asp Pro Asn Gly
 50 55 60
 Pro Met Tyr Tyr Lys Gly Val Tyr His Phe Phe Tyr Gln Tyr Asn Pro
 65 70 75 80
 Tyr Arg Ala Thr Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val
 85 90 95
 Ser Val Asp Leu Val Asn Trp Ser Ala Leu Glu Asn Ala Met Asp Pro
 100 105 110
 Asp Ser Ser Phe Asp Ile Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile
 115 120 125
 Leu Pro Asp Gly Thr Pro Val Phe Leu Tyr Thr Gly Ile Asp Ala Asp
 130 135 140
 Asn Asn Gln Val Gln Asn Val Ala Phe Pro Lys Asn Ala Ser Asp Pro
 145 150 155 160
 Leu Leu Arg Glu Trp Val Lys Pro Ser Tyr Asn Pro Val Ile Ala Leu
 165 170 175
 Pro Asp Asp Val Val His Asp Asn Phe Arg Asp Pro Ser Thr Ala Trp
 180 185 190
 Leu Gly Arg Asp Gly Leu Trp Arg Val Ala Val Ser Ala Gly Leu Lys
 195 200 205
 Asp Gly Thr Gly Thr Thr Leu Val Tyr Arg Ser Lys Asp Phe Arg Gln
 210 215 220
 Trp Glu Arg Asn Ala Glu Pro Leu Tyr Ser Ser Ser Asp Ala Gly Met
 225 230 235 240
 Val Glu Cys Pro Asp Leu Phe Pro Leu Ala Glu Pro Gly Asp Gln His
 245 250 255
 Gly Leu Asp Tyr Thr Pro Ser Asn Gly Ala Ala Val Ser Tyr Val Leu
 260 265 270
 Lys Gln Ser Val Met Asp Thr Leu Ser Asp Tyr Tyr Val Leu Gly Arg
 275 280 285
 Tyr Asp Asp Ala Ala Asp Thr Phe Ser Pro Val Glu Ala Asp Asn Asp
 290 295 300
 Cys Arg Thr Trp Gln Arg Phe Asp Tyr Gly His Val Tyr Ala Ser Lys
 305 310 315 320
 Ser Phe Tyr Asp Ala Gly Lys Lys Arg Arg Val Leu Trp Ser Trp Ala
 325 330 335
 Asn Glu Ser Asp Pro Glu Ala Asp Tyr Leu Ala Arg Gly Trp Ala Gly
 340 345 350
 Val Gln Ala Val Pro Arg Arg Ile Trp Leu Asp Ser Lys Gly Lys Gln
 355 360 365
 Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu Thr Leu Arg Lys Thr Arg
 370 375 380
 Val Gly Leu Leu Gly Ala Glu Met Asn Ala Gly Gly Met Asn Glu Ile
 385 390 395 400
 Ile Gly Val Ala Gly Ala Gln Ala Asp Val Glu Val Val Phe Glu Val
 405 410 415
 Pro Ser Leu Glu Gly Ala Glu Asn Leu Asp Pro Asn Gln Leu Leu Asp
 420 425 430
 Pro Gln Arg Leu Cys Gly Glu Lys Gly Ala Ser Val Leu Gly Gly Val
 435 440 445
 Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Gln Glu His
 450 455 460
 Thr Ser Val Phe Phe Arg Val Phe Arg His Glu Gly Lys Tyr Lys Val
 465 470 475 480
 Leu Met Cys Thr Asp Leu Arg Arg Ser Thr Thr Arg Ala Asp Val Tyr
 485 490 495
 Lys Pro Pro Tyr Gly Gly Phe Val Asp Ile Asp Ile Glu Lys Glu Arg
 500 505 510
 Ser Ile Ser Leu Arg Thr Leu Val Asp His Ser Val Val Glu Ser Tyr
 515 520 525
 Gly Gly Gly Gly Arg Thr Val Ile Thr Ala Arg Val Tyr Pro Glu His
 530 535 540

Ala Ala Thr Thr Asn Ser Arg Leu Phe Met Phe Asn Asn Gly Thr Gly
 545 550 555 560
 Ala Val Lys Val Ser Lys Leu Asp Ala Trp Glu Leu Ala Pro Ala Lys
 565 570 575
 Val Asn Val Pro Gly Asp Gly Leu Ile Thr Ala Gly Ser Ser Met His
 580 585 590
 Leu Arg Glu Ala Tyr
 595

<210> 82

<211> 399

<212> PRT

<213> Festuca arundinacea

<400> 82

Leu Asn Ser Thr Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro
 1 5 10 15
 Asp Gly Leu Trp Arg Ile Ala Ile Gly Ala Glu Leu Asn Gly Tyr Gly
 20 25 30
 Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Thr Arg Val
 35 40 45
 Asp His Pro Leu Tyr Ser Asp Asn Ala Pro Ser Met Trp Glu Cys Pro
 50 55 60
 Asp Phe Phe Ala Val Leu Pro Gly Asn Asn Gly Gly Leu Asp Leu Ser
 65 70 75 80
 Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu Lys Met Ser Val Asp
 85 90 95
 Tyr Ser Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Arg Asp Ala
 100 105 110
 Phe Val Pro Asp Val Val Leu Asp Asp Arg Arg Leu Trp Leu Arg Ile
 115 120 125
 Asp Tyr Gly Thr Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Arg
 130 135 140
 Gly Arg Arg Val Ile Trp Gly Trp Ser Asn Glu Thr Asp Ser Val Ser
 145 150 155 160
 Asp Asp Gly Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Ser
 165 170 175
 Ile Trp Leu Asp Ser Asp Gly Lys Gln Leu Leu Gln Trp Pro Ile Asp
 180 185 190
 Glu Ile Glu Ser Leu Arg Arg Asp Glu Ile Asn His Gln Gly Leu Glu
 195 200 205
 Leu Lys Asn Gly Asp Leu Phe Glu Ile Lys Gly Ile Asp Thr Leu Gln
 210 215 220
 Ala Asp Ile Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Ser Ala Asp
 225 230 235 240
 Pro Phe Asp Pro Ser Trp Leu Leu Asp Val Glu Arg His Cys Arg Glu
 245 250 255
 Ala Gly Ala Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val
 260 265 270
 Leu Ala Ser Asp Asn Met Glu Glu His Ile Ala Val His Phe Arg Val
 275 280 285
 Tyr Lys Ser Gln Lys Ser His Met Ile Leu Met Cys Ser Asp Leu Arg
 290 295 300
 Arg Ser Ser Leu Arg Ser Gly Leu Tyr Thr Pro Ala Tyr Gly Gly Phe
 305 310 315 320
 Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu
 325 330 335
 Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys
 340 345 350
 Ile Thr Ala Arg Ile Tyr Pro Val Ala Leu Val Asp Gly Arg Val His
 355 360 365
 Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu
 370 375 380
 Gly Ala Trp Ser Met Met Thr Ala Gln Val Asn Val Asn Lys Gly
 385 390 395

<210> 83
 <211> 583
 <212> PRT
 <213> Festuca arundinacea

<400> 83
 Met Gly Asn Pro Lys Trp Ile Phe Ala Pro Trp Ala Val Leu Leu Leu
 1 5 10 15
 Phe Leu Leu Gln Leu Ala Cys Ala Ser His His Thr Arg Arg Ser Leu
 20 25 30
 Glu Thr Glu Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro
 35 40 45
 Leu Leu Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn
 50 55 60
 Asp Pro Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr
 65 70 75 80
 Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His
 85 90 95
 Ser Val Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile
 100 105 110
 Thr Pro Ser Ile Pro Thr Asp Lys Tyr Gly Val Trp Ser Gly Ser Thr
 115 120 125
 Thr Ile Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp
 130 135 140
 Arg Pro Ser Ile Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn
 145 150 155 160
 Ala Ser Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro
 165 170 175
 Ile Ala Val Pro Val Ala Gly Met Asn Ala Thr Gln Phe Arg Asp Pro
 180 185 190
 Thr Thr Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly
 195 200 205
 Leu Arg Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Leu
 210 215 220
 Asp Phe Lys Asn Trp Thr Arg Ala His His Pro Leu His Ser Ala Leu
 225 230 235 240
 Thr Gly Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Glu Ala Gly
 245 250 255
 Val Glu Lys Gly Leu Asp Thr Ser Glu His Gly Glu Gly Val Glu Lys
 260 265 270
 His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
 275 280 285
 Val Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
 290 295 300
 Thr Gly Asp Val Tyr Arg Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
 305 310 315 320
 Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
 325 330 335
 Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
 340 345 350
 Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
 355 360 365
 Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
 370 375 380
 Gly Lys Pro Val Thr Val Gly Asp Lys Val Val Lys Pro Gly Gln His
 385 390 395 400
 Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
 405 410 415
 Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
 420 425 430
 Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Ala Asn
 435 440 445
 Gly Gly Val Gly Pro Phe Gly Leu Val Val Leu Ala Ser Ala Asp Leu
 450 455 460
 Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
 465 470 475 480

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<210> 84
<211> 346
<212> PRT
<213> Lolium perenne
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<400>	84																
Met	Tyr	Tyr	Asn	Gly	Ile	Tyr	His	Glu	Phe	Tyr	Gln	Tyr	Asn	Pro	Asn		
1				5					10					15			
Gly	Ser	Leu	Trp	Gly	Asn	Ile	Ile	Trp	Gly	His	Ser	Val	Ser	Thr	Asp		
			20					25					30				
Leu	Ile	Asn	Trp	Ile	Pro	Val	Glu	Pro	Ala	Ile	Glu	Arg	Asp	Ile	Pro		
		35					40					45					
Ser	Asp	Ile	Asn	Gly	Cys	Trp	Thr	Gly	Ser	Ala	Thr	Ile	Ile	Ser	Gly		
	50					55					60						
Asp	Gln	Pro	Ile	Ile	Ile	Tyr	Thr	Gly	Ala	Asp	Lys	Glu	Asn	Arg	Gln		
65				70						75					80		
Leu	Gln	Asn	Ile	Val	Leu	Pro	Lys	Asn	Lys	Ser	Asp	Pro	Tyr	Leu	Arg		
				85					90					95			
Glu	Trp	Thr	Lys	Ala	Gly	Asn	Asn	Pro	Val	Ile	Gln	Pro	Val	Gly	Pro		
			100					105					110				
Gly	Leu	Asn	Ala	Ser	Gln	Phe	Arg	Asp	Pro	Thr	Thr	Gly	Trp	Ile	Gly		
		115					120					125					
Pro	Asp	Gly	Leu	Trp	Arg	Ile	Ala	Val	Gly	Ala	Glu	Leu	Asn	Gly	Tyr		
	130					135					140						
Gly	Ala	Ala	Leu	Leu	Tyr	Lys	Ser	Gln	Asp	Phe	Leu	Asn	Trp	Thr	Arg		
145				150						155					160		
Val	Asp	His	Pro	Leu	Tyr	Ser	Ser	Asn	Ala	Ser	Ser	Met	Trp	Glu	Cys		
				165					170					175			
Pro	Asp	Phe	Phe	Ala	Val	Leu	Pro	Gly	Asn	Ser	Gly	Gly	Leu	Asp	Leu		
			180					185					190				
Ser	Ala	Glu	Ile	Pro	Asn	Gly	Ala	Lys	His	Val	Leu	Lys	Met	Ser	Leu		
		195					200					205					
Asp	Ser	Cys	Asp	Lys	Tyr	Met	Ile	Gly	Val	Tyr	Asp	Leu	Lys	Ser	Asp		
	210				215						220						
Thr	Phe	Met	Pro	Asp	Ser	Val	Leu	Asp	Asp	Arg	Arg	Leu	Trp	Ser	Arg		
225				230						235					240		
Ile	Asp	His	Gly	Asn	Phe	Tyr	Ala	Ser	Lys	Ser	Phe	Phe	Asp	Ser	Lys		
				245					250					255			
Lys	Gly	Arg	Arg	Ile	Ile	Trp	Gly	Trp	Thr	Asn	Glu	Thr	Asp	Ser	Ser		
			260					265					270				
Ser	Asp	Asp	Val	Ala	Lys	Gly	Trp	Ala	Gly	Ile	His	Ala	Ile	Pro	Arg		
		275					280					285					
Thr	Ile	Trp	Leu	Asp	Ser	Tyr	Gly	Lys	Gln	Leu	Leu	Gln	Trp	Pro	Ile		
	290					295					300						
Glu	Glu	Ile	Glu	Ser	Leu	Arg	Arg	Asn	Glu	Ile	Ser	His	Gln	Gly	Leu		
305				310													

<210> 85
 <211> 581
 <212> PRT
 <213> Festuca arundinacea

<400> 85
 Met Ala Gly Leu Arg Leu Ala Ala Val Ala Phe His Leu Cys Leu Leu
 1 5 10 15
 Leu Ser Pro Ser Ser Ser Leu Arg Arg Leu Tyr His Glu Asp Asp Glu
 20 25 30
 Ala Glu Ser Thr Pro Gly His Gly Gly Ser Arg Thr Ala Tyr His Phe
 35 40 45
 Gln Pro Ala Lys Asn Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
 50 55 60
 Asn Gly Leu Tyr His Leu Phe Tyr Gln Tyr Asn Pro Arg Gly Ala Thr
 65 70 75 80
 Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val Ser Val Asp Leu
 85 90 95
 Val Asn Trp Ala Ala Leu Asp Thr Ala Leu Asp Pro Asp Ser Pro Phe
 100 105 110
 Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Asp Gly
 115 120 125
 Gln Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Ala Gly Asn Gln Val
 130 135 140
 Gln Asn Val Ala Phe Pro Lys Lys Ala Ser Asp Pro Leu Leu Arg Glu
 145 150 155 160
 Trp Val Lys Pro Asp Tyr Asn Pro Val Ile Pro Leu Pro Lys Asp Val
 165 170 175
 Val His Asp Ser Phe Arg Asp Pro Ser Thr Ala Trp Arg Gly Arg Asp
 180 185 190
 Gly Leu Trp Arg Val Ala Ile Ala Ala Lys Val Asn Val Thr Val Thr
 195 200 205
 Val Gly Ser Thr Leu Ile Tyr Arg Ser Lys Asp Phe Arg Arg Trp Glu
 210 215 220
 Arg Asn Ala Ala Pro Leu Tyr Glu Ser Leu Ala Ala Gly Met Val Glu
 225 230 235 240
 Cys Pro Asp Leu Phe Pro Val Ala Lys Pro Gly Ala Gln Asn Gly Leu
 245 250 255
 Asp Tyr Ala Pro Ser Ser Arg Ala Ala Arg His Val Leu Lys Leu Ser
 260 265 270
 Val Val Ala Thr Leu Gln Asp Tyr Tyr Val Val Gly Leu Tyr Asp Asp
 275 280 285
 Thr Ala Asp Thr Phe Asn Ala Ala Ala Gly Ala Asp Asn Asp Trp Arg
 290 295 300
 Thr Trp Arg Arg Ile Asp Tyr Gly His Val Tyr Ala Ser Lys Ser Phe
 305 310 315 320
 Phe Asp Ala Arg Lys Asn Arg Arg Val Leu Trp Cys Trp Ala Asn Glu
 325 330 335
 Ser Asp Thr Glu Ala Asp Tyr Ile Ala Arg Gly Trp Ser Gly Val Gln
 340 345 350
 Thr Val Pro Arg Lys Ile Trp Leu Asp Ile Asp Gly Lys Gln Leu Leu
 355 360 365
 Gln Trp Pro Ile Lys Glu Ile Glu Thr Leu Arg Lys Lys Arg Val Gly
 370 375 380
 Leu Leu Gly Thr Glu Met Asn Ser Gly Gly Leu Asn Glu Ile Ile Gly
 385 390 395 400
 Val Ala Gly Ser Gln Ala Asp Val Glu Val Val Phe Lys Ile Pro Thr
 405 410 415
 Leu Glu Gly Ala Glu Asn Ile Glu Pro Asn Glu Leu Leu Asp Pro Gln
 420 425 430
 Lys Leu Cys Gly Asn Asn Gly Ala Ser Met Arg Gly Ser Ile Gly Pro
 435 440 445
 Phe Gly Leu Leu Leu Leu Ala Ser Gly Asp Leu Leu Glu His Thr Ser
 450 455 460
 Val Phe Phe Arg Val Phe Lys His Gly Ala Lys Tyr Lys Val Leu Met
 465 470 475 480

Cys Thr Asp Leu Thr Arg Ser Thr Thr Arg Ser Asp Val Tyr Lys Pro
 485 490 495
 Ser Tyr Gly Gly Phe Val Asp Met Asp Ile Asp Lys Thr Lys Ser Ile
 500 505 510
 Ser Leu Arg Thr Leu Ile Asp His Ser Val Val Glu Ser Phe Gly Gly
 515 520 525
 Gly Gly Arg Thr Cys Ile Thr Ala Arg Val Tyr Pro Glu His Ala Glu
 530 535 540
 Met Ser Asn Ser His Ile Tyr Met Phe Asn Asn Gly Thr Gly Ala Val
 545 550 555 560
 Lys Val Ala Lys Leu Glu Ala Trp Glu Leu Ala Thr Ala Asn Val Asn
 565 570 575
 Val Ala Gly His Gly
 580

<210> 86

<211> 588

<212> PRT

<213> Lolium perenne

<400> 86

Met Gly Val Arg Leu Gly Arg Val Ala Trp Ala Cys Pro Ala Val Leu
 1 5 10 15
 Val Leu Leu Leu Gln Leu Ala Gly Ala Ser His Val Val Tyr Glu Thr
 20 25 30
 Ser Leu Leu Glu Thr Glu Ala Ala Ala Thr Val Pro Ala Ser Ile
 35 40 45
 Phe Glu Leu Ser Thr Gly Tyr His Phe Arg Pro Gln Lys Asn Trp Ile
 50 55 60
 Asn Asp Pro Asn Ala Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe
 65 70 75 80
 Phe Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Val Trp Ala
 85 90 95
 His Ser Val Ser Arg Asp Leu Ile Asn Trp Val Ala Leu Glu Thr Ala
 100 105 110
 Leu Ala Pro Ser Ile Asp Ala Asp Lys Tyr Gly Cys Trp Ser Gly Ser
 115 120 125
 Ala Thr Ile Met Pro Asp Gly Thr Pro Val Ile Met Tyr Thr Gly Val
 130 135 140
 Ser Arg Pro Asp Val Asn Tyr Glu Val Gln Asn Val Ala Phe Pro Lys
 145 150 155 160
 Asn Ser Ser Asp Pro Leu Leu Arg Glu Trp Val Lys Pro Ala His Asn
 165 170 175
 Pro Val Ile Val Pro Glu Gly Gly Ile Asn Ala Thr Gln Phe Arg Asp
 180 185 190
 Pro Thr Thr Ala Trp Tyr Ala Asp Gly His Trp Arg Ile Leu Val Gly
 195 200 205
 Ala Leu Ser Gly Ala Ser Arg Gly Val Ala Tyr Val Tyr Arg Ser Arg
 210 215 220
 Asp Phe Arg Arg Trp Thr Arg Val Arg Lys Pro Leu His Ser Ala Pro
 225 230 235 240
 Thr Gly Met Trp Glu Cys Pro Asp Phe Tyr Pro Val Thr Val Asp Gly
 245 250 255
 Lys Glu Ser Gly Val Asp Thr Ser Val Val Ser Ser Ser Arg Val Lys
 260 265 270
 His Val Leu Lys Asn Ser Leu Asp Leu Arg Arg Tyr Asp Tyr Tyr Thr
 275 280 285
 Val Gly Thr Tyr Asp Arg Leu Lys Glu Arg Tyr Val Pro Asp Asn Pro
 290 295 300
 Ala Gly Asp Lys His His Leu Arg Tyr Asp Tyr Gly Asn Phe Tyr Ala
 305 310 315 320
 Ser Lys Thr Phe Tyr Asp Pro Ser Lys Arg Arg Arg Ile Leu Trp Gly
 325 330 335
 Trp Ala Asn Glu Ser Asp Thr Ala Val Asp Asp Val Ala Lys Gly Trp
 340 345 350

Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
 355 360 365
 Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Lys Ala Leu Arg Gly
 370 375 380
 Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
 385 390 395 400
 Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
 405 410 415
 Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
 420 425 430
 Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
 435 440 445
 Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
 450 455 460
 Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
 465 470 475 480
 Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
 485 490 495
 Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
 500 505 510
 Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
 515 520 525
 Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
 530 535 540
 Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
 545 550 555 560
 Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
 565 570 575
 Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
 580 585

<210> 87

<211> 668

<212> PRT

<213> Lolium perenne

<400> 87

Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala Ala Leu
 1 5 10 15
 Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg Thr Gly
 20 25 30
 Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu Ala
 35 40 45
 Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro Ala Gly
 50 55 60
 Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val Ser Gly
 65 70 75 80
 Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly Ala Ala
 85 90 95
 Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn Ala Phe
 100 105 110
 Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe
 115 120 125
 Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr
 130 135 140
 Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly Ala Ile
 145 150 155 160
 Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp Met Leu
 165 170 175
 Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp Tyr Asp
 180 185 190
 Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp Gly Arg
 195 200 205
 Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Val Gln
 210 215 220

Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr Asn Trp
 225 230 235 240
 Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His Val Gly
 245 250 255
 Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly Ser Asp
 260 265 270
 Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg Ala Gly
 275 280 285
 Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu Leu Val
 290 295 300
 Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu Cys Ile
 305 310 315 320
 Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr Glu Ala
 325 330 335
 Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His Val Met
 340 345 350
 Lys Glu Ser Ser Asp Asp Asp Arg His Asp Tyr Tyr Ala Leu Gly Arg
 355 360 365
 Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp Ala Asp
 370 375 380
 Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Lys
 385 390 395 400
 Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly Trp Val
 405 410 415
 Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp Ala Ser
 420 425 430
 Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr Gly Ser
 435 440 445
 Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg Thr Asn
 450 455 460
 Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val Phe Pro
 465 470 475 480
 Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg
 485 490 495
 Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val Gly Tyr
 500 505 510
 Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu Gly Pro
 515 520 525
 Phe Gly Leu Leu Val Leu Ala Asp Ala Arg Arg His Gly Gly Asp Thr
 530 535 540
 Glu Gln Thr Ala Val Tyr Phe Tyr Val Ala Arg Gly Leu Asp Gly Asn
 545 550 555 560
 Leu Arg Thr His Phe Cys His Asp Glu Ser Arg Ser Ser Arg Ala Asn
 565 570 575
 Asp Ile Val Lys Arg Val Val Gly Asn Ile Val Pro Val Leu Asp Gly
 580 585 590
 Lys Ala Leu Ser Val Arg Val Leu Val Ala His Ser Ile Val Glu Ser
 595 600 605
 Phe Ala Gln Gly Gly Arg Ser Val Val Thr Ser Arg Val Tyr Pro Thr
 610 615 620
 Glu Ala Ile Tyr Ala Asn Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr
 625 630 635 640
 Gly Ala Arg Val Pro Ala Thr Ser Leu Val Val His Lys Met Asp Pro
 645 650 655
 Ser Tyr Asn Gln Asn Gln Ala Glu Met Ala Ser Leu
 660 665

<210> 88

<211> 473

<212> PRT

<213> Lolium perenne

<400> 88

Val His Trp Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr
 1 5 10 15

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Asp Ile Asn Gly Val Trp Thr Gly Ser Ala Thr Val Phe Pro Asp Gly
      20      25      30
Thr Leu Asn Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Ala
      35      40      45
Gln Cys Leu Ala Val Pro Glu Asp Pro Asn Asp Ser Leu Leu Arg Asn
      50      55      60
Trp Thr Lys His Glu Ala Asn Pro Val Leu Leu Pro Pro Pro Gly Ile
      65      70      75      80
Gly Asp Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Phe Asp Glu Ser
      85      90      95
Asp Gln Thr Trp Arg Thr Val Ile Gly Ser Lys Asp Asn Asn Gly His
      100      105      110
Ala Gly Ile Ala Met Val Tyr Lys Thr Lys Asp Phe Leu Asn Tyr Glu
      115      120      125
Leu Ile Pro Gly Tyr Leu His Arg Val Asp Gly Thr Gly Met Trp Glu
      130      135      140
Cys Ile Asp Phe Tyr Pro Val Gly Gly Lys Asn Gly Ser Glu Glu Leu
      145      150      155      160
Tyr Val Ile Lys Glu Ser Ser Asp Asp Asp Arg His Asp Trp Tyr Thr
      165      170      175
Leu Gly Lys Tyr Asp Ala Ala Ala Asn Thr Phe Thr Ala Ala Asp Pro
      180      185      190
Glu Asn Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr
      195      200      205
Ala Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp
      210      215      220
Gly Trp Ile Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly
      225      230      235      240
Trp Ala Ser Leu Met Ser Ile Pro Arg Thr Val Glu Leu Asp Glu Lys
      245      250      255
Thr Trp Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Ile Glu Thr Leu
      260      265      270
Arg Ile Lys Ser Thr Asp Leu Gly Gly Ile Thr Ile Asp His Gly Ser
      275      280      285
Val Tyr Pro Leu Pro Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala
      290      295      300
Ser Phe Arg Leu Asp Ala Ala Thr Val Ala Ala Leu Asn Glu Ala Asp
      305      310      315      320
Val Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ser Thr His Arg Gly Ala
      325      330      335
Leu Gly Pro Phe Gly Ile Leu Val Leu Ala Asp Gly Lys Ala Glu Gln
      340      345      350
Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Leu Asp Gly Ala Leu Glu
      355      360      365
Thr His Phe Cys His Asp Glu Ser Arg Ser Thr Leu Ala Lys Asp Val
      370      375      380
Val Lys Arg Val Val Gly Tyr Thr Val Pro Val Leu Asp Gly Glu Ala
      385      390      395      400
Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val Glu Ser Phe Ala
      405      410      415
Met Gly Gly Arg Ser Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu Ser
      420      425      430
Ile Tyr Gly Ala Ala Gly Ala Tyr Leu Phe Asn Asn Ala Thr Gly Gly
      435      440      445
Ser Val Thr Val Glu Lys Leu Val Val His Glu Met Asp Ser Ser Tyr
      450      455      460
Asn Gln Ile Phe Met Ala Asp Asp Leu
      465      470

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<210> 89

<211> 539

<212> PRT

<213> Lolium perenne

<400> 89

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Ile Phe Arg Ser Arg Leu Pro Asp Ile Asp Ile Pro Thr His Met Pro
1      5      10      15
Leu His Asp Tyr Cys Phe Ala Thr Ala Ala Ser Ala Pro Asp Ala Pro
20     25     30
Cys Leu Ile Thr Ala Ala Thr Gly Arg Thr Tyr Thr Phe Ala Glu Thr
35     40     45
His Leu Leu Cys Arg Lys Ala Ala Ala Leu His Gly Leu Gly Val
50     55     60
Arg His Gly Asp Arg Ile Met Val Leu Leu Gln Asn Ser Val Glu Phe
65     70     75     80
Ala Leu Ala Phe Phe Gly Ala Ser Met Leu Gly Ala Val Ser Thr Ala
85     90     95
Ala Asn Pro Phe Cys Thr Pro Gln Glu Ile His Lys Gln Leu Val Ala
100    105    110
Ser Gly Ala Lys Leu Val Val Thr Gln Ser Ala Tyr Val Asp Lys Leu
115    120    125
Arg His Glu Ala Phe Pro Arg Ile Gly Glu Ala Leu Thr Val Ile Thr
130    135    140
Ile Asp Asp Asp Gly Thr Pro Asp Gly Cys Gln Pro Phe Trp Gly Leu
145    150    155    160
Val Ser Ala Ala Asp Glu Asn Ser Val Pro Glu Ser Pro Ile Ser Pro
165    170    175
Asp Asp Ala Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro
180    185    190
Lys Gly Val Val Leu Thr His Gly Gly Leu Val Ser Ser Val Ala Gln
195    200    205
Gln Val Asp Gly Glu Asn Pro Asn Leu His Met Arg Ala Gly Glu Asp
210    215    220
Val Val Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser
225    230    235    240
Val Leu Leu Cys Ala Leu Arg Ala Gly Ala Val Met Leu Met Pro
245    250    255
Arg Phe Glu Met Gly Ala Met Leu Glu Gly Ile Glu Arg Trp Arg Val
260    265    270
Thr Val Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn
275    280    285
Pro Gly Val Glu Lys His Asp Leu Ser Ser Ile Arg Ile Val Leu Ser
290    295    300
Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Gly Arg
305    310    315    320
Leu Pro Gln Ala Ile Phe Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly
325    330    335
Pro Val Leu Ser Met Cys Pro Ala Phe Ala Arg Glu Pro Thr Pro Ala
340    345    350
Lys Ser Gly Ser Cys Gly Thr Val Arg Asn Ala Glu Leu Lys Val
355    360    365
Val Asp Pro Asp Thr Gly Val Ser Leu Gly Arg Asn Leu Pro Gly Glu
370    375    380
Ile Cys Ile Arg Gly Pro Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro
385    390    395    400
Val Ala Thr Ala Ala Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly
405    410    415
Asp Ile Gly Tyr Val Asp Asp Asp Asp Glu Val Phe Ile Val Asp Arg
420    425    430
Val Lys Glu Leu Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu
435    440    445
Leu Glu Ala Leu Leu Ile Ala His Pro Ser Ile Ala Asp Ala Ala Val
450    455    460
Val Pro Gln Lys Asp Asp Ala Ala Gly Glu Val Pro Val Ala Phe Val
465    470    475    480
Val Arg Ala Ala Asp Ser Asp Ile Ala Glu Glu Ala Ile Lys Glu Phe
485    490    495
Val Ser Lys Gln Val Val Phe Tyr Lys Arg Leu His Lys Val Tyr Phe
500    505    510

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Thr His Ala Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Glu
 515 520 525
 Leu Arg Ala Lys Leu Ala Ala Pro Ala Thr Ala
 530 535

<210> 90
 <211> 559
 <212> PRT
 <213> Lolium perenne

<400> 90
 Met Gly Ser Ile Ala Ala Asp Leu Ala Pro Glu Ala Pro Ala Glu Leu
 1 5 10 15
 Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
 20 25 30
 Leu Gln Asp Tyr Cys Phe Glu Arg Leu Pro Glu Leu Ser Ala Arg Ala
 35 40 45
 Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
 50 55 60
 Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
 65 70 75 80
 Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
 85 90 95
 Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
 100 105 110
 Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Ala Ala
 115 120 125
 Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
 130 135 140
 Arg Ala Phe Ala Ala Glu Arg Gly Ile Pro Val Val Ser Val Asp Glu
 145 150 155 160
 Ala Val Asp Asp Gly Cys Leu Pro Phe Ala Ala Thr Leu Leu Gly Glu
 165 170 175
 Glu Ser Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
 180 185 190
 Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
 195 200 205
 Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
 210 215 220
 Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
 225 230 235 240
 Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
 245 250 255
 Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
 260 265 270
 Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
 275 280 285
 Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
 290 295 300
 Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
 305 310 315 320
 Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
 325 330 335
 Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
 340 345 350
 Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
 355 360 365
 Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
 370 375 380
 Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
 385 390 395 400
 Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
 405 410 415
 Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
 420 425 430

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Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
      435      440      445
Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
      450      455      460
Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
465      470      475      480
Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
      485      490      495
Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
      500      505      510
Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
      515      520      525
Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
      530      535      540
Leu Ala Ala Gly Ile Pro Gly Ser Asp Thr Thr Gln Ser Lys Asn
545      550      555

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<210> 91

<211> 559

<212> PRT

<213> Festuca arundinacea

<400> 91

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Met Gly Ser Ile Ala Ala Asp Ala Pro Glu Ala Pro Pro Ala Glu Leu
  1      5      10      15
Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
      20      25      30
Leu Gln Asp Tyr Cys Phe Gln Arg Leu Pro Glu His Ser Ala Arg Ala
      35      40      45
Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
      50      55      60
Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
      65      70      75      80
Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
      85      90      95
Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
      100      105      110
Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Thr Ala
      115      120      125
Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
      130      135      140
Arg Ala Phe Ala Ala Glu Arg Gly Ile Thr Val Val Ser Val Asp Glu
145      150      155      160
Gly Val Asp Asp Gly Cys Leu Pro Phe Gly Glu Thr Leu Leu Gly Glu
      165      170      175
Asp Gly Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
      180      185      190
Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
      195      200      205
Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
      210      215      220
Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
225      230      235      240
Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
      245      250      255
Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
      260      265      270
Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
      275      280      285
Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
      290      295      300
Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
305      310      315      320
Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
      325      330      335

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Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
 340 345 350
 Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
 355 360 365
 Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
 370 375 380
 Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
 385 390 395 400
 Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
 405 410 415
 Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
 420 425 430
 Val Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
 435 440 445
 Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
 450 455 460
 Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
 465 470 475 480
 Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
 485 490 495
 Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
 500 505 510
 Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
 515 520 525
 Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
 530 535 540
 Leu Ala Ala Gly Ile Pro Gly Ser Glu Thr Thr Gln Ser Lys Ser
 545 550 555

<210> 92

<211> 557

<212> PRT

<213> Lolium perenne

<400> 92

Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Thr Glu
 50 55 60
 Val Asp Tyr Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140
 Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155 160
 Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235 240

Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
 260 265 270
 Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
 275 280 285
 Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Gly Ala
 290 295 300
 Asp Asp Leu Ala Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
 305 310 315 320
 Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
 325 330 335
 Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
 340 345 350
 Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
 355 360 365
 Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
 370 375 380
 Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
 385 390 395 400
 Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
 405 410 415
 Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
 420 425 430
 Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
 435 440 445
 Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
 450 455 460
 Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
 465 470 475 480
 Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
 485 490 495
 Ser Glu Ile Thr Glu Asn Glu Ile Lys Gln Phe Val Ser Lys Glu Val
 500 505 510
 Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
 515 520 525
 Lys Asn Pro Ser Gly Lys Ile Val Arg Lys Asp Leu Arg Ala Arg Leu
 530 535 540
 Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
 545 550 555

<210> 93

<211> 557

<212> PRT

<213> Festuca arundinacea

<400> 93

Met Gly Ser Val Pro Glu Glu Ser Val Val Ala Ala Ala Val Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
 50 55 60
 Val Glu Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140

Val Leu Glu Phe Ala Ala Glu Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155
 Gly Lys Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Glu Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Phe Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235
 Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
 260 265 270
 Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
 275 280 285
 Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Thr Ala
 290 295 300
 Asp Asp Leu Thr Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
 305 310 315
 Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
 325 330 335
 Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
 340 345 350
 Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
 355 360 365
 Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
 370 375 380
 Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
 385 390 395
 Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
 405 410 415
 Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
 420 425 430
 Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
 435 440 445
 Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
 450 455 460
 Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
 465 470 475
 Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
 485 490 495
 Ser Glu Ile Thr Glu Asn Asp Ile Lys Gln Phe Val Ser Lys Glu Val
 500 505 510
 Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
 515 520 525
 Lys Asn Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Arg Leu
 530 535 540
 Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
 545 550 555

<210> 94

<211> 501

<212> PRT

<213> Lolium perenne

<400> 94

Met Glu Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
 1 5 10 15
 Ala Val Leu Ala Ile Ala Val Ala Lys Leu Ala Gly Lys Arg Phe Arg
 20 25 30
 Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
 35 40 45

Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Ile Ala Lys Arg
 50 55 60
 Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
 65 70 75 80
 Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
 85 90 95
 Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
 100 105 110
 Asn Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
 115 120 125
 Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
 130 135 140
 Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
 145 150 155 160
 Val Lys Ala Asp Pro Ala Phe Ala Thr Ala Gly Thr Val Ile Arg Arg
 165 170 175
 Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
 225 230 235 240
 Arg Cys Thr Asn Leu Thr Thr Lys Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
 325 330 335
 Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
 340 345 350
 Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
 355 360 365
 Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
 370 375 380
 Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
 385 390 395 400
 Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
 420 425 430
 Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Val Leu
 435 440 445
 Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
 450 455 460
 Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
 465 470 475 480
 Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
 485 490 495
 Lys Pro Leu Glu Ala
 500

<210> 95

<211> 505

<212> PRT

<213> Festuca arundinacea

<400> 95

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Met Asp Phe Val Phe Val Glu Lys Leu Leu Val Gly Leu Leu Ala Ser
 1          5          10          15
Val Val Val Ala Ile Val Val Ser Lys Ile Arg Gly Arg Lys Leu Arg
 20          25          30
Leu Pro Pro Gly Pro Ile Pro Val Pro Ile Phe Gly Asn Trp Leu Gln
 35          40          45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Ala Ala Met Ala Arg Lys
 50          55          60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
 65          70          75
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
 85          90          95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
100          105          110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
115          120          125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Gln
130          135          140
Gln Tyr Arg Ala Gly Trp Glu Ala Glu Ala Ala Phe Val Val Asp Asn
145          150          155
Val Arg Ala Asp Pro Lys Ala Ala Thr Asp Gly Val Val Leu Arg Arg
165          170          175
His Leu Gln Leu Met Met Tyr Asn Asn Met Tyr Arg Ile Met Phe Asp
180          185          190
Arg Arg Phe Glu Ser Met Asp Asp Pro Leu Phe Leu Arg Leu Arg Ala
195          200          205
Leu Asn Gly Glu Arg Ser Arg Leu Ala Gln Ser Phe Glu Tyr Asn Tyr
210          215          220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Gly Tyr Leu Gly
225          230          235
Leu Cys Glu Gln Val Lys Glu Thr Arg Leu Lys Leu Phe Lys Asp Tyr
245          250          255
Phe Leu Asp Glu Arg Lys Lys Leu Ala Ser Thr Lys Ser Met Asp Thr
260          265          270
Asn Gly Leu Lys Cys Ala Ile Asp His Ile Leu Glu Ala Gln Glu Lys
275          280          285
Gly Glu Ile Asn Glu Asp Asn Val Leu Tyr Ile Ile Glu Asn Ile Asn
290          295          300
Val Ala Ala Ile Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala
305          310          315
Glu Leu Val Asn His Pro Glu Ile Gln Gln Lys Leu Arg Asp Glu Met
325          330          335
Asp Ala Val Leu Gly Ala Gly His Gln Ile Thr Glu Pro Asp Thr His
340          345          350
Lys Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Leu Arg Leu Arg
355          360          365
Met Ala Ile Pro Leu Leu Val Pro His Met Asn Leu His Asp Ala Lys
370          375          380
Leu Ala Gly Tyr Asn Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala
385          390          395
Trp Phe Leu Ala Asn Asn Pro Glu Gln Trp Lys Arg Pro Asp Glu Phe
405          410          415
Arg Pro Glu Arg Phe Leu Glu Glu Glu Lys His Val Glu Ala Ser Gly
420          425          430
Asn Asp Phe Arg Phe Leu Pro Phe Gly Val Gly Arg Arg Ser Cys Pro
435          440          445
Gly Ile Ile Leu Ala Leu Pro Ile Leu Gly Ile Thr Ile Gly Arg Leu
450          455          460
Val Gln Asn Phe Glu Leu Thr Thr Pro Pro Gly Val Asp Lys Leu Asp
465          470          475
Thr Thr Glu Lys Gly Gly Gln Phe Ser Leu His Ile Leu Asn His Ser
485          490          495
Thr Ile Val Ala Lys Pro Arg Val Phe
500          505

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<210> 96
 <211> 361
 <212> PRT
 <213> Lolium perenne

<400> 96
 Met Gly Ile Val Asn Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45
 His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Pro Lys Tyr
 50 55 60
 Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
 65 70 75 80
 Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
 85 90 95
 Ile Val Gly Cys Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
 100 105 110
 Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
 115 120 125
 Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln
 130 135 140
 Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
 145 150 155 160
 Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
 165 170 175
 Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly
 180 185 190
 Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
 195 200 205
 Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp
 210 215 220
 Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
 225 230 235 240
 Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
 245 250 255
 His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
 260 265 270
 Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met
 275 280 285
 Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
 290 295 300
 Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr
 305 310 315 320
 Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu
 325 330 335
 Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
 340 345 350
 Gly Ser Asn Ile Asp Asp Thr Ala Ala
 355 360

<210> 97
 <211> 361
 <212> PRT
 <213> Festuca arundinacea

<400> 97
 Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Thr Thr Gly His Leu Ser Pro Tyr Thr Tyr Thr Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45

```

His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
 50      55      60
Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
65      70      75      80
Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
      85      90      95
Ile Val Gly Cys Cys His Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
      100      105      110
Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
      115      120      125
Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ala Met Val Val Asp Gln
      130      135      140
Lys Phe Ala Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
145      150      155      160
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
      165      170      175
Gly Leu Met Thr Pro Gly Leu Arg Gly Ile Leu Gly Leu Gly Gly
      180      185      190
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
      195      200      205
Thr Val Ile Ser Ser Ser Asn Lys Lys Arg Ala Glu Ala Met Asp Asp
      210      215      220
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
225      230      235      240
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
      245      250      255
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
      260      265      270
Val Leu Met Gly Val Ile Ala Glu Pro Leu Ser Phe Val Ser Pro Met
      275      280      285
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
      290      295      300
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Glu Lys Gly Leu Thr
305      310      315      320
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn His Ala Leu Glu
      325      330      335
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
      340      345      350
Gly Ser Asn Ile Lys Asp Ala Asp Ala
      355      360

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<210> 98

<211> 265

<212> PRT

<213> Lolium perenne

<400> 98

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Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Ala Lys Glu Gln
 1      5      10      15
Thr Thr Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
      20      25      30
Ser Glu Val Gly His Lys Ser Leu Leu Gln Ser Asp Ala Leu Tyr Gln
      35      40      45
Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
      50      55      60
Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
65      70      75      80
Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
      85      90      95
Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
      100      105      110
Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
      115      120      125
Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
      130      135      140

```

Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
 145 150 155 160
 Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Thr Phe Asp
 165 170 175
 Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
 180 185 190
 Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Leu Gly Tyr Asp Asn
 195 200 205
 Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
 210 215 220
 Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
 225 230 235 240
 Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
 245 250 255
 Gly Ile Thr Leu Cys Arg Arg Ala Lys
 260 265

<210> 99

<211> 265

<212> PRT

<213> Festuca arundinacea

<400> 99

Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Pro Lys Glu Gln
 1 5 10 15
 Pro Ala Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
 20 25 30
 Ser Glu Val Gly His Lys Ser Leu Gln Ser Asp Ala Leu Tyr Gln
 35 40 45
 Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
 50 55 60
 Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
 65 70 75 80
 Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
 85 90 95
 Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
 100 105 110
 Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
 115 120 125
 Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
 130 135 140
 Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
 145 150 155 160
 Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Ser Phe Asp
 165 170 175
 Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
 180 185 190
 Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Ile Gly Tyr Asp Asn
 195 200 205
 Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
 210 215 220
 Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
 225 230 235 240
 Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
 245 250 255
 Gly Ile Thr Leu Cys Arg Arg Ala Lys
 260 265

<210> 100

<211> 363

<212> PRT

<213> Lolium perenne

<400> 100

Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala
 1 5 10 15

```

Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala
      20      25      30
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly
      35      40      45
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala
      50      55      60
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys
      65      70      75      80
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys
      85      90      95
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln
      100      105      110
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala
      115      120      125
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly
      130      135      140
Ala Val Thr Met His Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu
      145      150      155      160
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr
      165      170      175
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg
      180      185      190
Gln Arg Gly Val Asp Leu Val Val Asn Pro Val Leu Val Ile Gly
      195      200      205
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys
      210      215      220
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr
      225      230      235      240
Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
      245      250      255
Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
      260      265      270
Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
      275      280      285
Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
      290      295      300
Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
      305      310      315      320
Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
      325      330      335
Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
      340      345      350
Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
      355      360

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<210> 101

<211> 342

<212> PRT

<213> Festuca arundinacea

<400> 101

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Met Thr Val Val Asp Ala Ala Ala Pro Gln Leu Pro Gly His Gly Gln
  1      5      10      15
Thr Val Cys Val Thr Gly Ala Ala Gly Tyr Ile Ala Ser Gly Leu Val
      20      25      30
Lys Leu Leu Leu Glu Arg Gly Tyr Thr Val Lys Gly Thr Val Arg Asn
      35      40      45
Pro Asp Asp Pro Lys Asn Ala His Leu Lys Ala Leu Asp Gly Ala Thr
      50      55      60
Glu Arg Leu Ile Leu Cys Lys Ala Asp Leu Leu Asp Tyr Asp Ala Ile
      65      70      75      80
Cys Ala Ala Val Glu Gly Cys His Gly Val Phe His Thr Ala Ser Pro
      85      90      95
Val Thr Asp Asp Pro Glu Gln Met Val Glu Pro Ala Val Arg Gly Thr
      100      105      110

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Glu Tyr Val Ile Asn Ala Ala Ala Asp Ala Gly Thr Val Arg Arg Val
 115 120 125
 Val Phe Thr Ser Ser Ile Gly Ala Ile Thr Met Asp Pro Asn Arg Gly
 130 135 140
 Pro Asp Val Val Val Asn Glu Ser Cys Trp Ser Asp Leu Glu Phe Cys
 145 150 155 160
 Lys Lys Thr Lys Asn Trp Tyr Cys Tyr Gly Lys Ala Val Ala Glu Gln
 165 170 175
 Ala Ala Trp Glu Ala Ala Arg Lys Arg Gly Ile Asp Leu Val Val Val
 180 185 190
 Asn Pro Val Leu Val Val Gly Pro Leu Leu Gln Pro Thr Val Asn Ala
 195 200 205
 Ser Ala Ala His Ile Leu Lys Tyr Leu Asp Gly Ser Ala Lys Lys Tyr
 210 215 220
 Ala Asn Ala Val Gln Ser Tyr Val Asp Val Arg Asp Val Ala Gly Ala
 225 230 235 240
 His Ile Arg Val Phe Glu Ala Pro Glu Ala Ser Gly Arg Tyr Leu Cys
 245 250 255
 Ala Glu Arg Val Leu His Arg Gly Asp Val Val Gln Ile Leu Ser Lys
 260 265 270
 Leu Phe Pro Glu Tyr Pro Val Pro Thr Arg Cys Ser Asp Glu Val Asn
 275 280 285
 Pro Arg Lys Gln Pro Tyr Lys Met Ser Asn Gln Lys Leu Gln Asp Leu
 290 295 300
 Gly Leu Gln Phe Thr Pro Val Asn Asp Ser Leu Tyr Glu Thr Val Lys
 305 310 315 320
 Ser Leu Gln Glu Lys Gly His Leu Leu Val Pro Ser Lys Pro Glu Gly
 325 330 335
 Leu Asn Gly Val Thr Ala
 340

<210> 102

<211> 360

<212> PRT

<213> Festuca arundinacea

<400> 102

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Gln Glu Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
 210 215 220

Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320
 Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Phe Glu Ala Leu Ala
 325 330 335
 Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
 340 345 350
 Ala Trp Ala Ile Glu Phe Thr Lys
 355 360

<210> 103

<211> 360

<212> PRT

<213> FLolium perenne

<400> 103

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Asp Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Val Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Ile Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Glu Gly Leu Gly Ser Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Thr Ile Lys Gly
 210 215 220
 Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Asn
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320

Asn	Pro	Gly	Gly	Arg	Glu	Arg	Tyr	Glu	Arg	Glu	Phe	Gln	Ala	Leu	Ala
				325					330					335	
Arg	Gly	Ala	Gly	Phe	Thr	Gly	Val	Lys	Ser	Thr	Tyr	Ile	Tyr	Ala	Asn
			340					345						350	
Ala	Trp	Ala	Ile	Glu	Phe	Thr	Lys								
		355					360								

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<210> 104
<211> 360
<212> PRT
<213> Festuca arundinacea
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<div><400></div>	<div>104</div>															
Met	Gly	Ser	Thr	Ala	Ala	Asp	Met	Thr	Ala	Ser	Ala	Asp	Glu	Glu	Ala	
1				5					10					15		
Cys	Met	Phe		Ala	Gln	Leu	Ala	Ser	Ser	Ser	Ile	Leu	Pro	Met	Thr	
			20					25					30			
Leu	Lys	Asn	Ala	Ile	Glu	Leu	Gly	Leu	Leu	Glu	Ile	Leu	Val	Ala	Ala	
		35					40					45				
Gly	Gly	Lys	Ser	Leu	Thr	Pro	Thr	Glu	Val	Ala	Ala	Lys	Leu	Pro	Ser	
	50					55					60					
Ala	Ala	Asn	Pro	Glu	Ala	Pro	Asp	Met	Val	Asp	Arg	Met	Leu	Arg	Leu	
65				70					75						80	
Leu	Ala	Ser	Tyr	Asn	Val	Val	Ser	Cys	Leu	Val	Glu	Glu	Gly	Lys	Asp	
				85					90					95		
Gly	Arg	Leu	Ser	Arg	Asn	Tyr	Gly	Ala	Ala	Pro	Val	Cys	Lys	Phe	Leu	
			100					105					110			
Thr	Pro	Asn	Glu	Asp	Gly	Val	Ser	Met	Ala	Ala	Leu	Ala	Leu	Met	Asn	
		115					120					125				
Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	Tyr	Leu	Lys	Asp	Ala	Val	
	130					135					140					
Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala	Phe	
145				150					155						160	
Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Arg	Val	Phe	Asn	Glu	Gly	
			165						170					175		
Met	Lys	Asn	His	Ser	Ile	Ile	Ile	Thr	Lys	Lys	Leu	Leu	Glu	Leu	Tyr	
			180					185					190			
Asp	Gly	Phe	Gln	Gly	Leu	Gly	Thr	Leu	Val	Asp	Val	Gly	Gly	Gly	Val	
		195					200					205				
Gly	Ala	Thr	Val	Ala	Ala	Ile	Thr	Ala	His	Tyr	Pro	Ala	Ile	Lys	Gly	
	210					215					220					
Val	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Ser	Glu	Ala	Pro	Pro	Phe	Pro	
225				230						235					240	
Gly	Val	Thr	His	Val	Gly	Gly	Asp	Met	Phe	Lys	Lys	Val	Pro	Ser	Gly	
			245						250					255		
Asp	Ala	Ile	Met	Met	Lys	Trp	Ile	Leu	His	Asp	Trp	Ser	Asp	Gln	His	
			260					265					270			
Cys	Ala	Thr	Leu	Leu	Lys	Asn	Cys	Tyr	Asp	Ala	Leu	Pro	Ala	His	Gly	
		275					280					285				
Lys	Val	Val	Leu	Val	Glu	Cys	Ile	Leu	Pro	Val	Asn	Pro	Glu	Ala	Lys	
	290					295					300					
Pro	Ser	Ser	Gln	Gly	Val	Phe	His	Val	Asp	Met	Ile	Met	Leu	Ala	His	
305				310						315					320	
Asn	Pro	Gly	Gly	Arg	Glu	Arg	Tyr	Glu	Arg	Glu	Phe	Glu	Ala	Leu	Ala	
			325													

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<210> 105
<211> 361
<212> PRT
<213> Lolium perenne
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<400> 105

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Met Gly Ser Thr Ala Ala Glu Ile Ala Ala Ser Ala Asp Glu Glu Ala
 1          5          10          15
Cys Leu Tyr Ala Leu Gln Leu Gly Ser Ser Ser Ile Leu Pro Met Thr
 20          25          30
Leu Lys Asn Thr Ile Glu Leu Gly Leu Leu Glu Thr Leu Met Ala Ala
 35          40          45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Cys
 50          55          60
Ala Ala Lys Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg
 65          70          75          80
Leu Leu Ala Ser Tyr Asn Leu Val Ser Cys Leu Val Glu Glu Gly Thr
 85          90          95
Asp Gly Arg Leu Ser Arg Arg Tyr Gly Ala Ala Pro Val Cys Lys Phe
100          105          110
Leu Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met
115          120          125
Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala
130          135          140
Val Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala
145          150          155          160
Phe Glu Tyr His Gly Thr Asp Leu Arg Phe Asn Arg Val Phe Asn Glu
165          170          175
Ala Met Lys Asn Asn Ser Ile Ile Ile Thr Lys Lys Leu Leu Gln Leu
180          185          190
Tyr Asp Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly
195          200          205
Val Gly Ala Thr Val Ala Ala Ile Thr Ala His Tyr Pro Thr Ile Lys
210          215          220
Gly Ile Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Pro Phe
225          230          235          240
Pro Gly Val Thr His Ile Gly Gly Asp Met Phe Lys Lys Val Pro Ser
245          250          255
Gly Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln
260          265          270
His Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Val His
275          280          285
Gly Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala
290          295          300
Lys Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala
305          310          315          320
His Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Tyr Glu Ala Leu
325          330          335
Ala Arg Gly Ala Gly Phe Ala Gly Phe Lys Ser Thr Tyr Ile Tyr Ala
340          345          350
Asn Ala Trp Ala Ile Glu Phe Thr Lys
355          360

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<210> 106

<211> 532

<212> PRT

<213> Lolium perenne

<400> 106

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Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Ile Gln Asp Pro Leu
 1          5          10          15
Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
 20          25          30
Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
 35          40          45
Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
 50          55          60
Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
 65          70          75          80
Lys Leu His Thr Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
 85          90          95

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Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
 130 135 140
 Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
 145 150 155 160
 Ala Leu Val Arg Ala Val Ala Arg Arg Thr Gly Glu Ser Val Asp Leu
 165 170 175
 Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
 180 185 190
 Phe Gly Ala Gly Ala Val Ala Ala Asp Ala Glu Glu Gly Asp Gly Ala
 195 200 205
 Gly Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu
 210 215 220
 Phe Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala
 225 230 235 240
 Asp Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Asn Ala Leu
 245 250 255
 Asp Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys
 260 265 270
 Asn Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe
 275 280 285
 Leu Pro Glu Ala Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp
 290 295 300
 Asp Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile
 305 310 315 320
 Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile
 325 330 335
 Glu Trp Ala Met Ala Glu Met Met His Ser Pro Asp Asp Leu Arg Arg
 340 345 350
 Leu Gln Gln Glu Leu Val Asp Val Val Gly Leu Asp Arg Asn Val Asp
 355 360 365
 Glu Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu
 370 375 380
 Thr Leu Arg Leu His Pro Pro Ile Pro Leu Leu His Glu Thr Ala
 385 390 395 400
 Glu Asp Cys Val Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val
 405 410 415
 Met Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Arg Ala Trp Lys Asp
 420 425 430
 Ala Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala
 435 440 445
 Ala Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly
 450 455 460
 Ser Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu
 465 470 475 480
 Glu Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro
 485 490 495
 Asp Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu
 500 505 510
 Thr Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu
 515 520 525
 Ala Cys Thr Gln
 530

<210> 107

<211> 542

<212> PRT

<213> Festuca arundinacea

<400> 107

Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Leu Gln Glu Pro Leu
 1 5 10 15

Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
 20 25 30
 Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
 35 40 45
 Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
 50 55 60
 Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
 65 70 75 80
 Lys Leu His Ala Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
 85 90 95
 Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
 130 135 140
 Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
 145 150 155 160
 Ala Leu Val Arg Ala Val Ala Arg Arg Ser Gly Glu Ser Val Asp Leu
 165 170 175
 Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
 180 185 190
 Phe Gly Ala Gly Ala Val Ala Gly Asp Gly Asp Gly Asp Gly Ala Gly
 195 200 205
 Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu Phe
 210 215 220
 Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala Asp
 225 230 235 240
 Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Ala Ala Leu Asp
 245 250 255
 Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys Asn
 260 265 270
 Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe Leu
 275 280 285
 Pro Glu Thr Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp Asp
 290 295 300
 Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile Ile
 305 310 315 320
 Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile Glu
 325 330 335
 Trp Ala Met Ala Glu Met Met His Ser Pro Gly Asp Leu Arg Arg Leu
 340 345 350
 Gln Gln Glu Leu Ala Asp Val Val Gly Leu Asp Arg Asn Val Asp Glu
 355 360 365
 Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu Thr
 370 375 380
 Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala Glu
 385 390 395 400
 Asp Cys Ile Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val Met
 405 410 415
 Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Lys Ala Trp Lys Asp Ala
 420 425 430
 Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala Ala
 435 440 445
 Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly Ser
 450 455 460
 Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu Glu
 465 470 475 480
 Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro Asp
 485 490 495
 Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu Thr
 500 505 510
 Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu Ala
 515 520 525
 Cys Thr Gln Leu Leu Gly Ala Asp Asp Ala Gly Arg Gln Ala
 530 535 540

<210> 108
 <211> 711
 <212> PRT
 <213> Lolium perenne

<400> 108
 Met Glu Ser Glu Asn Val Ala Ala Asn Gly Asp Gly Leu Cys Val Ala
 1 5 10 15
 Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala Glu Glu
 20 25 30
 Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu Glu Tyr
 35 40 45
 Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile Ala Met
 50 55 60
 Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu Asp Glu
 65 70 75 80
 Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met Asn Ser
 85 90 95
 Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
 100 105 110
 Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg Glu Leu
 115 120 125
 Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp Gly His
 130 135 140
 Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg Val Asn
 145 150 155 160
 Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Thr
 165 170 175
 Val Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro Leu Arg
 180 185 190
 Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
 195 200 205
 Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro Asp Gly
 210 215 220
 Thr Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile Gln His
 225 230 235 240
 Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val Asn Gly
 245 250 255
 Thr Ala Val Gly Ser Gly Leu Ala Ser Met Val Leu Phe Glu Ala Asn
 260 265 270
 Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys Glu Val
 275 280 285
 Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys Leu Lys
 290 295 300
 His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu
 305 310 315 320
 Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu Leu Asp
 325 330 335
 Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
 340 345 350
 Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr Lys Ser
 355 360 365
 Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
 370 375 380
 Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro Ile
 385 390 395 400
 Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
 405 410 415
 Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn
 420 425 430
 Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Tyr
 435 440 445
 Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
 450 455 460

Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
 465 470 475 480
 His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
 485 490 495
 Ser Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe Leu Val
 500 505 510
 Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Val Lys
 515 520 525
 Asn Ala Val Lys Asn Cys Val Lys Met Val Ala Arg Lys Thr Leu Ser
 530 535 540
 Thr Asn Asp Ser Gly His Leu His Ser Ala Arg Phe Cys Glu Lys Asp
 545 550 555 560
 Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala Asp Asp
 565 570 575
 Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala Val Leu
 580 585 590
 Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Arg Asp Val Gln Thr
 595 600 605
 Ser Val Phe Ala Lys Leu Ala Ala Phe Glu Gln Glu Leu Arg Ala Val
 610 615 620
 Leu Pro Arg Glu Val Glu Ser Ala Arg Cys Ala Val Glu Asn Gly Thr
 625 630 635 640
 Ala Ala Gln Gln Asn Arg Ile Thr Glu Cys Arg Ser Tyr Pro Leu Tyr
 645 650 655
 Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly Glu Lys
 660 665 670
 Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala Met Asn
 675 680 685
 Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu Trp Asn
 690 695 700
 Gly Glu Pro Leu Pro Ile Cys
 705 710

<210> 109

<211> 713

<212> PRT

<213> Festuca arundinacea

<400> 109

Met Glu Cys Glu Asn Gly His Val Ala Ala Asn Gly Asp Gly Leu Cys
 1 5 10 15
 Val Ala Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala
 20 25 30
 Glu Glu Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu
 35 40 45
 Glu Tyr Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile
 50 55 60
 Ala Met Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu
 65 70 75 80
 Asp Glu Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met
 85 90 95
 Asn Ser Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe
 100 105 110
 Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg
 115 120 125
 Glu Leu Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp
 130 135 140
 Gly His Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg
 145 150 155 160
 Val Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu
 165 170 175
 Glu Thr Ile Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro
 180 185 190
 Tyr Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
 195 200 205

```

Ile Ala Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro
 210          215          220
Asp Gly Ser Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile
225          230          235          240
Gln His Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val
          245          250          255
Asn Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu
          260          265          270
Ala Asn Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys
          275          280          285
Glu Val Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys
          290          295          300
Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ile Met Glu His
305          310          315          320
Ile Leu Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu
          325          330          335
Leu Asp Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr
          340          345          350
Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr
          355          360          365
Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
          370          375          380
Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
385          390          395          400
Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
          405          410          415
Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
          420          425          430
Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
          435          440          445
Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
          450          455          460
Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
          465          470          475          480
Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
          485          490          495
Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
          500          505          510
Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
          515          520          525
Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
          530          535          540
Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
          545          550          555          560
Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
          565          570          575
Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
          580          585          590
Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
          595          600          605
Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
          610          615          620
Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
          625          630          635          640
Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
          645          650          655
Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
          660          665          670
Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
          675          680          685
Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
          690          695          700
Trp Asn Gly Glu Pro Leu Pro Ile Cys
705          710

```

<210> 110
 <211> 323
 <212> PRT
 <213> Festuca arundinacea

<400> 110
 Met Ala Phe Ser Gly Ser Val Ser Gly Val Val Leu Val Val Ala Ile
 1 5 10 15
 Leu Leu Leu Gly Leu Ala Ala Ala Ser Ala Gln Leu Ser Ala Thr
 20 25 30
 Phe Tyr Asp Ala Ser Cys Pro Ser Ala Leu Ala Thr Ile Lys Ser Ala
 35 40 45
 Val Thr Ala Ala Val Asn Asn Glu Ala Arg Met Gly Ala Ser Leu Leu
 50 55 60
 Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Ala Ser Val
 65 70 75 80
 Leu Leu Asn Asp Thr Ala Asn Phe Thr Gly Glu Gln Thr Ala Phe Pro
 85 90 95
 Asn Arg Asn Ser Ile Arg Gly Leu Asn Val Ile Asp Asn Val Lys Ala
 100 105 110
 Gln Val Glu Ala Val Cys Thr Gln Thr Val Ser Cys Ala Asp Ile Leu
 115 120 125
 Ala Val Ala Ala Arg Asp Ser Ile Val Ala Leu Gly Gly Pro Ser Tyr
 130 135 140
 Thr Val Pro Leu Gly Arg Arg Asp Ser Thr Thr Ala Ser Leu Ser Glu
 145 150 155 160
 Ala Asn Arg Asp Leu Pro Pro Pro Ser Ser Asp Leu Ala Asp Leu Val
 165 170 175
 Gly Asn Phe Ser Arg Lys Gly Leu Ser Val Thr Asp Met Val Ala Leu
 180 185 190
 Ser Gly Ala His Thr Ile Gly Arg Ala Ala Cys Leu Asn Phe Arg Ser
 195 200 205
 Arg Ile Tyr Gly Glu Ser Asn Ile Ala Pro Ala Tyr Ala Ala Ser Leu
 210 215 220
 Gln Ala Asn Cys Pro Gln Ser Ala Pro Asn Gly Asp Gly Thr Leu Ala
 225 230 235 240
 Pro Leu Asp Val Ser Thr Pro Asp Ala Phe Asp Asn Ala Tyr Tyr Gly
 245 250 255
 Asn Leu Leu Ser Gln Gln Gly Leu Leu His Ser Asp Gln Gln Leu Phe
 260 265 270
 Asn Gly Gly Ser Thr Asp Ser Leu Val Ser Thr Tyr Ala Ser Asn Ala
 275 280 285
 Ala Gln Phe Ser Gly Asp Phe Ala Ala Ala Met Val Asn Met Gly Asn
 290 295 300
 Ile Gly Val Leu Thr Gly Ala Gln Gly Glu Ile Arg Leu Asn Cys Gly
 305 310 315 320
 Lys Val Asn

<210> 111
 <211> 344
 <212> PRT
 <213> Lolium perenne

<400> 111
 Met Ala Ser Ser Ser Pro Phe Ser Arg Val Ser Gln Leu Ala Val
 1 5 10 15
 Lys Ala Thr Val Leu Ala Ala Val Cys Leu Leu Leu His Gly Gly Gly
 20 25 30
 Gly Ser Ser Ala Ser Ala Ala Glu Leu Cys Val Ser Tyr Tyr Asp His
 35 40 45
 Thr Cys Pro Asp Ala Tyr Lys Ile Val Gln Gly Val Leu Val Glu Ala
 50 55 60
 His Lys Ser Asp Pro Arg Ile Phe Ala Ser Leu Ile Arg Leu His Phe
 65 70 75 80

His Asp Cys Phe Val Leu Gly Cys Asp Gly Ser Leu Leu Leu Asp Thr
 85 90 95
 Phe Pro Gly Phe Gln Ser Glu Lys Asp Ala Arg Pro Asn Asn Asn Ser
 100 105 110
 Ala Arg Gly Tyr Pro Val Val Asp Ala Ala Lys Ala Ala Leu Glu Lys
 115 120 125
 Ala Cys Pro Gly Val Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala
 130 135 140
 Glu Ile Ser Val Gln Leu Ser Gly Gly Pro Gly Trp Gly Val Leu Leu
 145 150 155 160
 Gly Arg Leu Asp Gly Lys Thr Ser Ser Ile Ala Gly Ala Gln Asn Leu
 165 170 175
 Pro Gly Pro Phe Asp Gly Leu Lys Asn Leu Thr Leu Lys Phe Gln Ala
 180 185 190
 Val Asn Leu Asp Val Thr Asp Leu Val Ala Leu Ser Gly Ala His Thr
 195 200 205
 Phe Gly Arg Val Lys Cys Arg Phe Val Thr Asn Arg Leu Tyr Asn Phe
 210 215 220
 Ser Gly Thr Asn Gln Pro Asp Pro Thr Leu Asn Ala Ala Tyr Arg Ala
 225 230 235 240
 Phe Leu Ser Thr Arg Cys Pro Arg Asn Gly Asp Ala Asn Ser Leu Asn
 245 250 255
 Asp Leu Asp Pro Thr Thr Pro Asp Thr Phe Asp Lys Asn Tyr Phe Thr
 260 265 270
 Asn Leu Glu Lys Asn Arg Gly Phe Leu Asp Ser Asp Gln Gln Leu Lys
 275 280 285
 Ser Asp Pro Gly Ala Leu Thr Thr Thr Ala Pro Ile Val Asp Arg Phe
 290 295 300
 Ala Ser Ser Gln Asp Ala Phe Phe Lys Ser Phe Ala Trp Ser Met Ile
 305 310 315 320
 Lys Met Gly Asn Ile Leu Pro Ile Thr Asp Pro Ser Arg Gly Glu Val
 325 330 335
 Arg Lys His Cys Ala Phe Val Asn
 340

<210> 112

<211> 326

<212> PRT

<213> Festuca arundinacea

<400> 112

Met Ala Thr Arg Gly Val Met Val Ala Leu Leu Leu Ala Ala Val Ala
 1 5 10 15
 Ala Ser Cys Ala His Ala Gln Leu His Glu Lys Phe Tyr Ser Glu Ser
 20 25 30
 Cys Pro Ser Val Glu Asp Val Val Arg Lys Glu Met Val Met Ala Leu
 35 40 45
 Ser Leu Ala Pro Ser Leu Ala Ala Pro Leu Leu Arg Met His Phe His
 50 55 60
 Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp Ser Ala
 65 70 75 80
 Asn Lys Thr Ala Glu Lys Asp Ala Leu Pro Asn Gln Thr Leu Arg Gly
 85 90 95
 Phe Asp Phe Val Glu Arg Val Lys Ala Ala Val Glu Lys Ala Cys Pro
 100 105 110
 Asp Thr Val Ser Cys Ala Asp Val Thr Leu Ile Ala Arg Asp Ala
 115 120 125
 Val Trp Leu Ser Lys Gly Pro Phe Trp Glu Val Pro Leu Gly Arg Arg
 130 135 140
 Asp Gly Ser Val Ser Ile Ser Asn Glu Thr Asp Ala Leu Pro Pro Pro
 145 150 155 160
 Thr Ala Asn Ile Thr Val Leu Thr Gln Leu Phe Ala Ala Lys Asn Leu
 165 170 175
 Asp Ile Lys Asp Leu Val Val Leu Ser Ala Ala His Thr Ile Gly Thr
 180 185 190

Ser His Cys Phe Ser Phe Ser Asp Arg Leu Tyr Asn Phe Thr Gly Leu
 195 200 205
 Asp Asn Ala Ser Asp Ile Asp Pro Thr Leu Glu Pro Phe Tyr Met Ala
 210 215 220
 Lys Leu Lys Ser Lys Cys Thr Ser Leu Asp Asp Asn Ser Thr Leu Val
 225 230 235 240
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Asp Tyr Phe Lys
 245 250 255
 Leu Val Ser Lys Arg Arg Gly Leu Phe His Ser Asp Gly Ala Leu Leu
 260 265 270
 Thr Asp Ala Phe Thr Arg Ala Tyr Ile Leu Arg His Ala Thr Gly Ala
 275 280 285
 Phe Lys Asp Glu Phe Phe Ala Asp Phe Ala Val Ser Met Val Lys Met
 290 295 300
 Gly Asn Thr Asp Val Leu Thr Gly Ser Gln Gly Glu Ile Arg Lys Lys
 305 310 315 320
 Cys Ser Val Val Asn His
 325

<210> 113

<211> 358

<212> PRT

<213> Lolium perenne

<400> 113

Met Ala Ser Ser Arg Val Leu Leu Leu Val Val Ala Ala Leu Ala Ile
 1 5 10 15
 Ser Val Ser Ala Thr Ala Ala Ala Thr Lys Ile Ser Ala Pro Leu Pro
 20 25 30
 Pro Leu Ala Lys Gly Leu Asn Phe Asp Phe Tyr Lys Ala Thr Cys Pro
 35 40 45
 Gln Ala Glu Ser Ile Val Phe Asn Phe Leu Arg Asp Ala Ile Arg Lys
 50 55 60
 Asp Val Gly Leu Ala Ala Ala Leu Leu Arg Ile His Phe His Asp Cys
 65 70 75 80
 Phe Val Gln Gly Cys Asp Gly Ser Val Leu Asp Lys Thr Gly Gly
 85 90 95
 Thr Asp Ser Glu Lys Ile Ala Pro Pro Asn Val Thr Leu Arg Pro Thr
 100 105 110
 Ala Phe Lys Ala Ile Asn Asp Leu Arg Ala Leu Leu Ala Lys Ala Cys
 115 120 125
 Gly Ala Val Val Ser Cys Ala Asp Ile Ala Ala Leu Ala Ala Arg Asp
 130 135 140
 Ser Val His Leu Ala Gly Gly Pro His Tyr Pro Val Pro Leu Gly Arg
 145 150 155 160
 Arg Asp Gly Leu Ala Pro Ala Asn Leu Thr Thr Ile Leu Asn Ala Leu
 165 170 175
 Pro Ala Pro Ser Ser Asn Val Thr Thr Leu Leu Arg Phe Leu Ala Lys
 180 185 190
 Ile Ser Leu Asp Ala Asn Asp Leu Val Ala Leu Ser Gly Ala His Thr
 195 200 205
 Leu Gly Ile Ala His Cys Thr Ser Phe Gln Glu Arg Leu Phe Pro Gln
 210 215 220
 Asn Asp Val Thr Leu Asn Lys Trp Phe Ala Ser Gln Leu Arg Leu Thr
 225 230 235 240
 Cys Pro Ala Leu Asn Thr Asp Asn Thr Thr Asn Asn Asp Ile Arg Thr
 245 250 255
 Pro Asn Val Phe Asp Asn Lys Tyr Tyr Val Asp Leu Leu Asn Arg Gln
 260 265 270
 Gly Leu Phe Thr Ser Asp Gln Asp Leu His Thr Asp Ala Arg Thr Lys
 275 280 285
 Pro Thr Val Thr Arg Phe Ala Val Asp Gln Ala Ala Phe Phe Asp Gln
 290 295 300
 Phe Val Phe Ser Val Val Lys Met Gly Gln Ile Asn Val Leu Thr Gly
 305 310 315 320

[illegible]

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<210> 114
<211> 344
<212> PRT
<213> Lolium perenne
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<400>	114															
Met	Thr	Thr	Met	Gly	Gly	Ser	Ser	Ile	Leu	Pro	Ala	Pro	Thr	Val	Ala	
1				5					10					15		
Thr	Thr	Ala	Leu	Val	Leu	Leu	Ile	Val	Leu	Phe	Ala	Ser	Pro	Ala	Thr	
			20					25					30			
Val	Ala	Lys	Gly	Ser	Gly	Leu	Ser	Val	Gly	Phe	Tyr	Lys	Lys	Leu	Cys	
		35					40					45				
Pro	Lys	Ala	Glu	Lys	Val	Val	Arg	Arg	Thr	Val	Thr	Lys	Ala	Phe	Glu	
	50					55					60					
Lys	Glu	Pro	Gly	Thr	Pro	Ala	Asp	Ile	Ile	Arg	Leu	Phe	Phe	His	Asp	
65					70					75					80	
Cys	Phe	Val	Arg	Gly	Cys	Asp	Ala	Ser	Val	Leu	Leu	Glu	Ser	Thr	Pro	
			85						90					95		
Gly	Arg	Met	Ala	Glu	Arg	Asp	Ser	Lys	Ala	Asn	Asn	Pro	Ser	Leu	Asp	
			100					105					110			
Gly	Phe	Glu	Val	Ile	Ser	Asp	Ala	Lys	Glu	Thr	Leu	Glu	Lys	Leu	Cys	
		115					120					125				
Pro	Gln	Thr	Val	Ser	Cys	Ala	Asp	Ile	Leu	Ala	Leu	Ala	Ala	Arg	Asp	
	130					135					140					
Gly	Ala	Tyr	Leu	Ala	Ser	Gly	Leu	Asp	Tyr	Ala	Val	Pro	Thr	Gly	Arg	
145					150					155					160	
Arg	Asp	Gly	Leu	Val	Ser	Lys	Glu	Asp	Glu	Val	Leu	Pro	Ser	Val	Pro	
			165						170					175		
His	Pro	Asp	Phe	Asn	His	Ser	Gln	Leu	Val	Glu	Asn	Phe	Thr	Ala	Lys	
			180					185					190			
Gly	Phe	Thr	Ala	Glu	Glu	Met	Val	Thr	Leu	Ser	Gly	Ala	His	Thr	Ile	
		195					200					205				
Gly	Thr	Ser	His	Cys	Ser	Ser	Phe	Thr	Asp	Arg	Leu	Tyr	Asn	Phe	Ser	
	210					215					220					
Gln	Gly	Gly	Ala	Leu	Thr	Thr	Asp	Pro	Ala	Leu	Pro	Ala	Ala	Tyr	Ala	
225					230					235					240	
Ala	Leu	Leu	Lys	Glu	Lys	Cys	Pro	Pro	Glu	Thr	Ala	Ala	Gln	Asn	Asp	
			245						250					255		
Thr	Thr	Met	Val	Gln	Leu	Asp	Asp	Val	Thr	Pro	Phe	Val	Met	Asp	Asn	
			260					265					270			
Gln	Tyr	Tyr	Lys	Asn	Leu	Leu	Ala	Gly	Thr	Val	Pro	Leu	Gly	Ser	Asp	
		275					280					285				
Val	Ala	Leu	Met	Glu	Ser	Pro	Asp	Thr	Ala	Ala	Leu	Val	Glu	Leu	Tyr	
	290					295					300					
Ala	Arg	Glu	Pro	Ala	Glu	Tyr	Trp	Ala	Lys	Arg	Phe	Val	Ala	Ala	Met	
305					310					315					320	
Val	Lys	Val	Ser	Glu	Met	Glu	Val	Leu	Thr	Gly	Ala	Glu	Gly	Glu	Ile	
			325						3							

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<210> 115
<211> 293
<212> PRT
<213> Lolium perenne
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```
<400> 115
Thr Arg Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu Thr
  1           5           10           15
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```

Ile Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly
      20      25      30
Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys
      35      40      45
Asp Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys
      50      55      60
Gly Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp
      65      70      75      80
Lys Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys
      85      90      95
Ala Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu Gly
      100      105      110
Gly Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr Ala
      115      120      125
Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn Leu
      130      135      140
Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr Asp
      145      150      155      160
Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
      165      170      175
Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala Phe
      180      185      190
Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly Asn
      195      200      205
Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly Tyr
      210      215      220
Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln Ala
      225      230      235      240
Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala Ser
      245      250      255
Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys Leu
      260      265      270
Ser Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val Asn
      275      280      285
Cys Arg Ala Val Asn
      290

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<210> 116

<211> 311

<212> PRT

<213> Festuca arundinacea

<400> 116

```

Met Ala Ser Ala Ser Cys Ile Ser Leu Val Leu Leu Val Ala Leu Ala
  1      5      10      15
Ala Thr Ala Ala Ser Ala Gln Leu Ser Ser Thr Phe Tyr Asp Thr Ser
      20      25      30
Cys Pro Arg Ala Leu Ala Thr Ile Lys Ser Gly Val Ala Ala Ala Val
      35      40      45
Ser Ser Asn Pro Arg Met Gly Ala Ser Leu Leu Arg Leu His Phe His
      50      55      60
Asp Cys Phe Val Asn Gly Cys Asp Ala Ser Val Leu Leu Ser Gly Asn
      65      70      75      80
Glu Gln Asn Ala Pro Ala Asn Ala Gly Ser Leu Phe Gly Phe Gly Val
      85      90      95
Ile Asp Asn Ile Lys Thr Gln Leu Glu Gly Ile Cys Lys Gln Thr Val
      100      105      110
Ser Cys Ala Asp Ile Leu Thr Val Ala Ala Arg Asp Ser Val Val Ala
      115      120      125
Leu Gly Gly Pro Ser Trp Thr Val Pro Leu Gly Arg Arg Asp Ser Thr
      130      135      140
Ser Ala Thr Gly Asn Thr Gly Asp Leu Pro Gly Pro Gly Ser Ser Leu
      145      150      155      160
Ala Gln Leu Gln Ala Ala Phe Ala Lys Lys Asn Leu Asn Thr Val Asp
      165      170      175

```

Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
 180 185 190
 Asn Phe Arg Ser Arg Ile Tyr Gly Gly Asp Ser Asn Ile Asn Ala Ala
 195 200 205
 Phe Ala Thr Ser Leu Lys Ala Asn Cys Pro Gln Ser Gly Gly Asn Gly
 210 215 220
 Asn Leu Ala Ala Leu Asp Ala Thr Thr Ala Asn Ala Phe Asp Asn Ala
 225 230 235 240
 Tyr Tyr Thr Asn Leu Leu Ser Gln Lys Gly Leu Leu His Ser Asp Gln
 245 250 255
 Val Leu Phe Asn Asn Gly Ser Thr Asp Asn Thr Val Arg Asn Phe Ala
 260 265 270
 Ser Ser Gly Ala Ala Phe Ser Ser Ala Phe Ala Thr Ala Met Ile Lys
 275 280 285
 Met Gly Asn Ile Ser Pro Leu Thr Gly Thr Gln Gly Gln Ile Arg Leu
 290 295 300
 Ser Cys Ser Lys Val Asn Ser
 305 310

<210> 117

<211> 230

<212> PRT

<213> Lolium perenne

<400> 117

Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
 1 5 10 15
 Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
 20 25 30
 Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
 35 40 45
 Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Thr Lys
 50 55 60
 Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
 65 70 75 80
 Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Thr Pro Val Thr Met
 85 90 95
 Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
 100 105 110
 Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asn Ala Glu Ala
 115 120 125
 Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Arg Thr Glu Ser Phe Pro
 130 135 140
 Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
 145 150 155 160
 Val Ala Phe Ser Lys Asp Ser Ser Val Pro Glu Ser Gly Gly Val Ala
 165 170 175
 Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Glu Ser Ile Ile Gly
 180 185 190
 Glu His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
 195 200 205
 Ala Glu Leu Leu Asn Glu Ala Ala Pro Val Gly Gln Ala Ala Ala Glu
 210 215 220
 Pro Val Ser Val Ser Ala
 225 230

<210> 118

<211> 231

<212> PRT

<213> Festuca arundinacea

<400> 118

Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
 1 5 10 15
 Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
 20 25 30

```

Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
      35      40      45
Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Ala Lys
      50      55      60
Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
      65      70      75      80
Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Arg Arg Val Thr Met
      85      90      95
Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
      100      105      110
Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asp Ala Glu Ala
      115      120      125
Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Lys Ala Glu Ser Phe Pro
      130      135      140
Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
      145      150      155      160
Val Ala Phe Ser Lys Asp Ser Ser Leu Pro Glu Ser Gly Gly Val Ala
      165      170      175
Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Lys Ser Ile Ile Gly
      180      185      190
Lys His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
      195      200      205
Ala Glu Leu Leu Lys Glu Ala Ala Pro Val Gly Glu Pro Ala Val Ala
      210      215      220
Glu Pro Val Ser Val Ser Ala
      225      230

```

<210> 119

<211> 394

<212> PRT

<213> Lolium perenne

<400> 119

```

Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
      1      5      10      15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
      20      25      30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
      35      40      45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
      50      55      60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
      65      70      75      80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
      85      90      95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
      100      105      110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
      115      120      125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
      130      135      140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
      145      150      155      160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
      165      170      175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
      180      185      190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
      195      200      205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
      210      215      220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
      225      230      235      240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
      245      250      255

```

Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
 260 265 270
 Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
 275 280 285
 Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
 290 295 300
 Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
 305 310 315 320
 Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
 325 330 335
 Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
 340 345 350
 Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
 355 360 365
 Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
 370 375 380
 Val Val Leu His Ser Met Pro Ile Ala Ala
 385 390

<210> 120

<211> 196

<212> PRT

<213> Festuca arundinacea

<400> 120

Met Tyr Phe Val Ser Lys Ser Leu Ala Glu Asn Ala Ala Met Asp Tyr
 1 5 10 15
 Ala Lys Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val
 20 25 30
 Val Gly Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala
 35 40 45
 Leu Ala Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln
 50 55 60
 Val Gln Leu Val His Leu Asp Asp Leu Cys Asp Ser Met Thr Tyr Leu
 65 70 75 80
 Phe Glu His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp
 85 90 95
 Thr Thr Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu
 100 105 110
 Tyr Asp Ile Pro Gln Lys Phe Pro Gly Ala Asp Asp Asp Leu Gln Pro
 115 120 125
 Ile His Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg
 130 135 140
 Tyr Thr Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu
 145 150 155 160
 Lys Gly Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser
 165 170 175
 Ala Ala Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile
 180 185 190
 Gly Ala Glu Thr
 195

<210> 121

<211> 329

<212> PRT

<213> Lolium perenne

<400> 121

Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
 1 5 10 15
 Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
 20 25 30
 Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
 35 40 45
 His Leu Leu Ala Leu Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
 50 55 60

Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
 65 70 75 80
 Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asn
 85 90 95
 Leu Val Leu Asn Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
 100 105 110
 Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
 115 120 125
 Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
 130 135 140
 Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
 145 150 155 160
 Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
 165 170 175
 Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
 180 185 190
 Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
 195 200 205
 Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
 210 215 220
 Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
 225 230 235 240
 Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
 245 250 255
 Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
 260 265 270
 Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
 275 280 285
 Pro Gly Leu Val Arg Ala Lys Ala Val Pro Lys Lys Leu Met Ala Leu
 290 295 300
 Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
 305 310 315 320
 Ser Leu Lys Ser Arg Gly Cys Ile Ala
 325

<210> 122

<211> 328

<212> PRT

<213> Lolium perenne

<400> 122

Gly Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe Val
 1 5 10 15
 Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His Val Ile
 20 25 30
 Gly Thr Val Arg Asp Pro Gly Asn Arg Arg Lys Val Gly His Leu Trp
 35 40 45
 Lys Leu Pro Gly Ala Asn Glu Arg Leu Gln Leu Val Arg Ala Asp Leu
 50 55 60
 Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Arg Ala Cys Glu Gly Val
 65 70 75 80
 Phe His Ile Ala Ser Pro Val Leu Gly Lys Ser Asp Ser Asn Cys Lys
 85 90 95
 Glu Ala Thr Leu Gly Pro Ala Ile Asn Gly Thr Leu Asn Val Leu Arg
 100 105 110
 Ser Cys Lys Lys Ser Pro Phe Leu Lys Arg Val Val Leu Thr Ser Ser
 115 120 125
 Ser Ser Ala Val Arg Ile Arg Asp Glu Thr Gln Gln Pro Glu Leu Leu
 130 135 140
 Trp Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys Leu Gln
 145 150 155 160
 Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala Leu Asp
 165 170 175
 Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Thr Val Leu Pro Ser Phe
 180 185 190

Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Thr Thr Ala Ser Asp
 195 200 205
 Ile Leu Gly Leu Leu Gln Gly Asp Thr Asp Arg Phe Thr Leu Tyr Gly
 210 215 220
 Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Ser His Ile Leu
 225 230 235 240
 Val Tyr Glu Thr Pro Glu Ala Thr Gly Arg Tyr Leu Cys Ser Ser Val
 245 250 255
 Val Leu Asp Asn Asn Glu Leu Val Gly Leu Leu Ala Lys Gln Phe Pro
 260 265 270
 Val Phe Pro Ile Pro Arg Arg Leu Lys Asn Pro Tyr Gly Lys Gln Ala
 275 280 285
 Tyr Gln Leu Asp Thr Ser Lys Leu Gln Gly Leu Gly Leu Lys Phe Lys
 290 295 300
 Gly Val Gln Glu Met Phe Asn Asp Cys Val Glu Ser Leu Lys Asp Gln
 305 310 315 320
 Gly His Leu Leu Glu Cys Pro Leu
 325

<210> 123

<211> 369

<212> PRT

<213> Lolium perenne

<400> 123

Met Ala Pro Val Val Glu Arg Ala Pro Phe Leu Pro Thr Gly Glu Ala
 1 5 10 15
 Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro Lys Val
 20 25 30
 Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu His Gly
 35 40 45
 Ile Asp Asp Ala Arg Arg Thr Glu Ile Arg Asp Arg Val Ala Ala Ala
 50 55 60
 Cys Glu Gly Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Ala
 65 70 75 80
 Ala Leu Ile Ala Glu Met Ala Arg Leu Ser Arg Asp Phe Phe Ala Leu
 85 90 95
 Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly Gly Lys Lys Gly
 100 105 110
 Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr Val Gln Asp Trp
 115 120 125
 Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys Ala Arg Asp Tyr
 130 135 140
 Gly Arg Trp Pro Asp Lys Pro Ala Gly Trp Arg Ala Val Val Glu Gln
 145 150 155 160
 Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu Leu Gly Val Leu
 165 170 175
 Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser Lys Ala Cys Val
 180 185 190
 Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro Lys Cys Pro Gln
 195 200 205
 Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
 210 215 220
 Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln Ala Thr Arg Asp
 225 230 235 240
 Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Ile Ala Gly Ala Phe Val
 245 250 255
 Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
 260 265 270
 Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser Ser Arg Leu Ser
 275 280 285
 Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Lys Val Trp Pro Leu
 290 295 300
 Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu Pro Ile Thr Phe
 305 310 315 320

Thr Glu Met Tyr Arg Arg Lys Met Ala Arg Asp Leu Glu Leu Ala Lys
 325 330 335
 Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln Gln Leu Gln Gln
 340 345 350
 Glu Ala Ala Pro Ala Ala Ala Pro Thr Lys Pro Leu Asn Gln Ile Leu
 355 360 365
 Ala

<210> 124

<211> 380

<212> PRT

<213> Festuca arundinacea

<400> 124

Met Ala Ser Val Glu Asn Ala Pro Phe Leu Pro Thr Ala Ala Thr Gly
 1 5 10 15
 Glu Ala Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro
 20 25 30
 Lys Val Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu
 35 40 45
 His Gly Ile Asp Asp Gly Gly Ala Arg Arg Ala Glu Ile Arg Asp Arg
 50 55 60
 Val Ala Ala Ala Cys Glu Gly Trp Gly Val Phe Gln Val Val Asp His
 65 70 75 80
 Gly Val Asp Ala Ala Leu Val Ala Glu Met Ala Arg Leu Ser Arg Glu
 85 90 95
 Phe Phe Ala Leu Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly
 100 105 110
 Gly Lys Lys Gly Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr
 115 120 125
 Val Gln Asp Trp Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys
 130 135 140
 Ala Arg Asp Tyr Gly Arg Trp Pro Glu Lys Pro Ala Gly Trp Arg Ala
 145 150 155 160
 Val Val Glu Gln Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu
 165 170 175
 Leu Gly Val Leu Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser
 180 185 190
 Lys Ala Cys Val Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro
 195 200 205
 Lys Cys Pro Gln Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp
 210 215 220
 Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln
 225 230 235 240
 Ala Thr Arg Asp Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Val Pro
 245 250 255
 Gly Ala Phe Val Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn
 260 265 270
 Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser
 275 280 285
 Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Glu Ala Lys
 290 295 300
 Val Trp Pro Leu Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu
 305 310 315 320
 Pro Ile Thr Phe Thr Glu Met Tyr Arg Arg Lys Met Ala Cys Asp Leu
 325 330 335
 Glu Leu Ala Lys Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln
 340 345 350
 Gln Leu Gln Gln Glu Gln Gln Glu Ala Val Ala Ala Ala Pro Lys
 355 360 365
 Pro Ala Thr Thr Lys Pro Leu Asn Gln Ile Leu Ala
 370 375 380

<210> 125
 <211> 2105
 <212> DNA
 <213> *Lolium perenne*

<400> 125
 acttagcctt cctcggaaacc atcgaccggg cgcgcgccga cgcgacgcga cgcgatggag 60
 tccagcgccg tcgtccccgg caccacggcg ccgctgcttc cttatgcgta cgcgcgcgtg 120
 ccgtogtcct ccgacgacgc ccgtgaaaac agaagtagcg gcggcgtagg gtggcgcgcg 180
 tgcgcgcggc ttctggcggc ctcggcgttg gcggtggttg tcgtggtcgg gctcctcgcg 240
 ggcggcaggg tggatcgggt cccggccggc gcagacgtgg cgtcggccac ggtgccggcc 300
 gtgccgatgg agttcccgag gagccggggc aaggacttgg cgtgtcggga gaagtcctcc 360
 ggtgcctact ccgcccagcg cgggttcccc tggagcaacg ccatgctgca gtggcagcgc 420
 accgggttcc atttccagcc ggagcagcac tacatgaacg atcccaacgg ccccggtgac 480
 tacggcggat ggtaccacct cttctaccag cacaacccca agggcgacag ctggggcaac 540
 atgcgcctggg cccacgcccgt gtccaaggac atggtcaact ggcgccacct cccgctcgcc 600
 atggttcccc accagtggta cgacagcaac ggcgtcctca ccggtcccat caccgtgctc 660
 cccgacggcc aggtcatcct gctctacacc ggcaacaccg acaccctagc ccaggctccag 720
 tgctcgcca cgcccggca cccgtccgac ccgctcctcc gcgaatggat caagcaccoc 780
 gccaaaccca tcctcttccc gccgcccggg atcgggtcga aggacttccg cgaccgctc 840
 accgcctggt tcgaccactc cgaccacacc tggcgccaccg tcatcgggtc caaggacgac 900
 gacggccacg ccggcatcat cctcagctac aagaccaagg acttcgtcaa ctacgagctc 960
 atgcccggga acatgcaccg ggggcccggc ggcaccggca tgtacgagtg catcgacctc 1020
 taccocgtcg gcggcaactc gtcggagatg ctcggcgggc acgactcgcc cgacgtgctc 1080
 ttcgtgctca aggagagcag cgatgacgaa cgtcacgact actatgcgct cggaagggtc 1140
 gacgcccgtc ccaacgtttg gacgcccacg gaccgggacc tggaccttgg gatcgggctc 1200
 agatacgact ggggaaagta ctacgctccc aagtccttct acgaccagaa gaagaaccgc 1260
 cgcacgttat ggcatacat cggcgagacc gactccgagc aggccgacat caccaaggga 1320
 tgggccaatc tcatgacgat tccaagaacg gtggagcttg acaggaagac ccgcacaaac 1380
 ctcatccaat ggccagtggg ggaggtcgac accctccgca ggaactccac ggacctcggt 1440
 cgcacacccg tcaacgcccg ctccgtcatt cgcctcccc tccaccaggg cgctcaactc 1500
 gacatcgagg cctccttcca actcaactct tccgacgtgg atgctatcaa cgaggccgac 1560
 gtcggctaca actgcagcac cagcggtgcc gcgtagcggg ggcgctcgg cccctttggc 1620
 ctccctcgcc ttgccaatgg ccgcaccgaa cagacggctg tgtacttcta cgtgtccaag 1680
 ggcgtcgacg ggggcctcca gaccacttt tgccacgacg agtcacggtc aacacgggca 1740
 aaggatgtcg tgaataggat gattggcagc atcgtgccgg tgcttgacgg tgagaccttt 1800
 tcggtgaggg tgctagtggg ccactccatc gtgcagagct tcgcatggg cgggaggatc 1860
 accggcgact cgccggcgta cccgacggag gccatctacg cggccgcagg ggtctacctc 1920
 ttcaacaacg ccacgggccc caccgtcacc gccgagaggc tcgtcgtgca cgagatggcc 1980
 tcagctgaca accatatctt caogaacgac gacttgtaga tgaaccaag tttagctcgt 2040
 gttgcattct tgtaacggc cgggtgattgc ctatctacac attcatttgg cgttcaaaaa 2100
 aaaaa 2105

<210> 126
 <211> 2068
 <212> DNA
 <213> *Festuca arundinacea*

<400> 126
 cccatccacc ggagtatact aggaatttcc tgcaactcga cctcgcgttg ggaattccgg 60
 caatggagtc ccgggccttt cccaacgcgg cgtacgcgcc acttctgcca cccaccgctg 120
 acgacgccac cctgggcaag caggaccgcc ccggcgtagg gtggcgcggg ttcttaaccg 180
 tgctggccgc gtctggcgtg gtggtgctcc tcgtcgtcgc cactatgctc gcgggatcca 240
 ggatgggtca ggcaggcgac accgacgagg acggggccgg agggttcccg tggagcaacg 300
 agatgctgca gtggcagcgc gccgggttcc attaccagcc cgaggggcac ttcatgagcg 360
 atccagacgg tccggtatac taccgtggat attaccacct cttctttcag tacaaccgaa 420
 ggggcgtcgc gtgggatgac tacatagagt ggggccaagt ggtgtcccag gacctgtac 480
 actggcgccc tctccactg gccctgcggc ctgaccattg gtacgacaag aaggcgctct 540
 tgtcgggtac catcacggtg ctccacaatg gcacgctcgt cctgctctac acgggggtca 600
 cagaagaccc tatggccgag tctcagtgca tcgcccgtcc gaccgacccc aacgaccccc 660
 tccttcgcca ttggaccaag cccccgcga accctgttct cgctcaccca cagggggtcc 720
 agggcatgga cttccgagac cccaccagtg catggtttga caagtccgac gccactggc 780
 gcatttctat cggttccaag gatgacgaca atggaagcca cgctggcatc gccttcatct 840
 tcaagaccaa ggacttcctt agcttcgagc gcgtcccagg tatcgtgcat cgtgtcgagg 900
 gtaccggtat gtgggagtg atcgactttt accccgtcgg aggtggccac aactcttcgt 960
 cggaggagct gtacgtgata aaggcgagca tggacgacga acgacacgac tactactcat 1020

tgaggagata	tgacgaggca	gccaacacat	ggacgccatt	ggacgcccag	ctagacttgg	1080
ggattgggct	gagatacgac	tgaggcaagc	tctacgctgc	cacgtcggtc	tacgatccgc	1140
tgaagcagcg	gcgaattatg	ttggggatat	taggcgagac	cgactctgca	cgagcccagc	1200
ttgccaagg	atggggcctca	cttcagtcga	ttccgaggac	agtgaacta	gacgagaaga	1260
ccaggacgaa	cctcctccta	tgggcgggtg	aggaggtgga	ggccctccgc	tacaactcca	1320
ccgacctcag	tggcatcact	gttgacaacg	gctcagtcct	ccacctcccc	ctccaccaag	1380
ccactcagct	ggacatcgag	gcttccttcc	gcctcgacgc	ttctgacgtt	gccgccatca	1440
acgaggccga	tgctcggtat	aactgcagca	gcagcggtgg	cgcgcccgca	cgtggcgcta	1500
tcggcccctt	cgccctcctc	gtccatgccc	ccggagacct	ccgtggcgag	cagacggcgg	1560
tgtactttcta	cgtgtccagg	gccctcgacg	gtaccctccg	gactagcttc	tgcaacgacg	1620
agacgcggtc	gtcacgggccc	agggacgtga	cgaagcgggt	ggtgggcagc	acggtgcccg	1680
tgctccacgg	tgaggcggtg	tcgatgagg	tgctcgtgga	ccactccatc	gtgcagagct	1740
tcgccatggg	tgggagagtc	acggcgacct	cgcggtgtga	cccaacggag	gccatctacg	1800
ccaggcgagg	gggttacctg	ttcaacaacg	ctaccggcgc	cagcgtgact	gcggagaggc	1860
tcctcgtgca	cgagatggcc	tcggcggtat	acgacgagac	cctgatcatg	gttgaggact	1920
cgtagctgct	cacatgagct	atatatcaga	ccggtaacgt	tggttcactt	gcattttcaa	1980
gcgttgaata	atttacttag	cttagcaagc	aacaggtccg	aggttccaag	taaggtgtgg	2040
gatatcttct	caaaattcaa	aaaaaaaa				2068

<210> 127

<211> 2198

<212> DNA

<213> *Lolium perenne*

<400> 127

cacccatcca	ccggaatata	tatactagcc	aggaaattcc	tgcaactcga	cctcgagttg	60
ggaattccgg	caatggagtc	ccgggccttt	cccagcgccg	cgtacgcgcc	acttctgcca	120
tcgcgcgag	acgacgtcgc	cctggccaag	caggaccgcc	ccggcggtgg	gtggcgccgg	180
ttcttaacgg	tgctggccgc	ctgcggcggt	gtgggtgctcc	tcgtcggtgc	cactttgctc	240
gcgggatcca	ggatgggtca	ggcaggcgac	ggcgaaggca	acaccgacga	ggatggggcc	300
ggagggttcc	cgtggagcaa	cgagatgctg	cagtggcgac	gcgcggggtt	ccattaccag	360
ccggaggggg	acttcatgag	cgatccaaac	ggtccagtat	actaccgcgg	atattaccac	420
ctcttctttc	agtacaaccg	aaggggcgtc	gcgtgggatg	actacataga	gtggggccac	480
gtggtgtccc	aggacctggg	acactggcgc	cctctcccac	tgcccatgcg	gcctgaccat	540
tggtacgaca	agaaggcggt	cttgctcggt	accatcacgg	tgctccacaa	tggcacgctc	600
gtcctgctct	acacgggggt	cacagaagac	cctatggccg	agtcccagtg	catcgccgct	660
ccgaccgacc	ccaacgaccc	cctccttcgc	cattggacca	agcaccgccg	caaccgcgtc	720
ctcgctcacc	cacagggggt	ccagggcgatg	gacttccgag	accccaccag	cgcgtgggtg	780
gacaagtccg	atgccacgtg	gcgcattctc	atcggttcca	aggacgacga	caacggcgac	840
cacgctggca	tcgccttcat	cttcaagact	aaggacttcc	ttagcttcga	gcgtgtccca	900
ggtatcggtc	atcggttcga	gggcaccggc	atgtgggagt	gcatcgactt	ttaccccgtc	960
ggaggtggcc	acaactcttc	gtcggaggag	ttgtacgtga	taaaggcgag	catggacgac	1020
gaaccgacg	actactactc	attggggagg	tacgagcgcg	cagcgaacac	atggacgcca	1080
ttggacgcgg	agctagactt	ggggattggg	ctgagatacg	actggggcaa	gctctacgct	1140
tcacgctcgt	tctacgatcc	ggtgaagcag	cggcgcatta	tggtggggta	tgtaggcgag	1200
gtcgaactct	cgcgagccga	tggtgccaag	ggatgggcct	cgcttcagtc	gattccgagg	1260
acagtggcgc	tagacgagaa	gacccgaacg	aacctcctcc	tatggccggg	ggaggagggtg	1320
gaggccctcc	gctacaactc	caccgacctc	agcggcatca	ccattgacaa	cggctccgct	1380
ttccacctcc	cactccacca	gaccactcag	ctggacatcg	aggcttcctt	ccgcctcgac	1440
gcttctgatg	ttgccggccat	caacgaggcc	gacgtcggtc	acaactgcag	cagcagcggc	1500
ggcgcgcgcg	cacgtggcgc	tctcgccccc	ttcggcctcc	tcgtccatgc	cgccggagac	1560
ctccgtggcg	agcagacggc	ggtctacttc	tacgtgtcca	gggccctcga	cgttaccctc	1620
cggaccagct	cttgcaacga	cgagacggcg	tcgtcgcggg	ccaggggacgt	gacgaagcgg	1680
gtggtgggca	gcacgggtgcc	ggtgctcgac	ggcgaggcgt	tgctgatgag	agtgtcgtg	1740
gaccactcca	tcgtgcagag	cttcgcgatg	ggcgggagga	ccacggcgac	ctcgcgcggtg	1800
taccgcagcg	aggccatcta	cgccagggct	ggggtgtacc	tggtcaacaa	cgccaccggc	1860
gccggcggtg	cggcgagag	gctcatcggt	cacgagatgg	cctcgcggtg	atagcagcag	1920
accctcatgg	ttgaggactc	atagctgctc	accgtaacg	ttgggtcact	tgcatttcca	1980
agcgttgaat	taataattta	cttgtttgtg	cagcaagcaa	cggctccgag	ttccaagtaa	2040
ggtgggatat	tctaccaaac	tccgcgagtc	ccgcaagggt	gtgtagggtg	gagttgatgt	2100
tggcgcacct	gcgcgtgtgc	atgtaagttg	ttgtatttgt	tggtctttta	aaaaagaaag	2160
ataccaatct	accatactat	gtaagcataa	aaaaaaaa			2198

<210> 128
 <211> 2208
 <212> DNA
 <213> *Lolium perenne*

<400> 128
 caccatcca ccggagtata ctagctagga aattcctgtg caactcgacc tcgagtttgg 60
 aattccggca atggagtccc gggactttcc cagcgcgccg tacgcgccac ttctgccatc 120
 tgccgcagac gacgtcgccc tggccaagca ggaccgcccc ggcgtggggg ggcgcggcct 180
 cttaaccgtg ctggccgcct gcggcgtggg ggtgtcctc gtcgctgcct ctttgcctgc 240
 ggggtccagg atgggtcagg caggcgacac cgacgaggac ggggcccagg ggttcccgtg 300
 gagcaacgag atgctgcagt ggcagcgccg cgggttccat taccagccgg aggggcactt 360
 catgagcgat ccagacgggt cgttatacta cgtggatat taccacctct tctttcagta 420
 caaccgaaga ggggtcgctg gggatgacta catagagtgg ggccacgtgg tgtcccagga 480
 cctggtacac tggcgccctc tcccactggc catgcccgtt gaccattggt acgacaagaa 540
 gggcgctctt tcgggtacca tcacggtgct ccacaatggc acgctcgtcc tcctctacac 600
 ggggttcaca gaagacccta tggccgagtc ccagtgcata gccgtcccga ccgaccccaa 660
 cgacccccct cttcgccatt ggaccaagca ccccgccaac cccgttctcg ctcacccaca 720
 ggggtccag ggcattggact tccgagaccc caccagcgcg tgggtgggaca agtccgactc 780
 caggtggcgc attctcatcg gttccaagga cgacgacaac ggcagccacg ctggcatcgc 840
 cttcatcttc aagaccaagg acttccttag cttcgagcgt gtcccaggta tcgtgcatcg 900
 tgtcgagggt accggcatgt gggagtgcata cgacttttac cccgttggag gtggccacaa 960
 ctcttcgtcg gaggagtgtg acgtgataaa ggcgagcatg gacgacgaac gacacgacta 1020
 ctactcattg gggaggtatg acgcgacagc gaacacatgg acgccattgg acgccgagct 1080
 agacttgggg attgggctga ggtacgactg gggcaagctc tacgcttcca cgtcgttcta 1140
 cgatccactg aagcagcggc gaattatggt ggggtatgta ggcgaggtcg actctgcgcg 1200
 agccgacgtt gccaaaggat gggcctcact tcagtcgatt ccgaggacag tggcactaga 1260
 cgagaagacc cggacgaacc tcctcctatg gccggtggag gagggtggag ccctccgcta 1320
 caactccacc gacctcagcg gcatcactgt tgagaacggc tccatcttcc acctccctct 1380
 ccaccaagcc actcagctgg acatcgaggc ttcttccgc ctogatgctt ctgatgttgc 1440
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 tggcgctctc gggcccttcg gcctcctcgt ccatgccgcc ggagacctcc gtggcgagca 1560
 gacggcggtg tacttctaog tgtccagggc cctcgagcgt agcctccgga ccagctctcg 1620
 caacgcagag acgcggtcgt cacgggcccg ggacgtgacg aagcgggtgg tgggcagcac 1680
 ggtgccggtg ctgcagggcg aggtgttagc gatgagggtg ctcgtaggac actcgatcgt 1740
 gcagagcttc gcgatgggtg ggagggtcac ggcgacgtcg cgggtgtacc caacggaggc 1800
 tatctacgcc agggcagggg tgtacctgtt caacaacgcc accggcgcca gcgtgacggc 1860
 ggagaggctc atcgtgcacg agatggcctc tggcgatcac ggcgtagacc tcatgtttaa 1920
 ggactcatag ctgctcacac atgagctatc agaccggtaa cgttgggtca ctagcatttt 1980
 caagcggtga aataatttac ttggcgtagc aagccccggg tccgagggtt caaaagtaag 2040
 gtgggatatt cttccaaact ccgcgagtcg cgcaagggtt tctaggtgtg agtgtgatgt 2100
 cgtttgcgca cctgcgcgtg tgcctgtaaa ttgctggatt tgttgtttct ttacagaaaa 2160
 aaaaggatac tatactatgt aagtatctac attgttgtaa aaaaaaaa 2208

<210> 129
 <211> 1790
 <212> DNA
 <213> *Festuca arundinacea*

<400> 129
 caccaacgaa attcgggagg aagaaaggcg ctccgccatc tctcccgaaa caaccgctcg 60
 ccaccgctct ccctcccctg ccctcgccct cccattcccc ttctcttctt tccttggcg 120
 acggcctcgt cgatcggaac caatctccac caaacgcgcc tccggatctc gcgcgcgcgc 180
 tcgaagggga tcctcccgtg gccgcgctcc tcctccgcgc ctccgctgga ctgtcgtgga 240
 gcggggatcg acccgggctc tctgtcgtcg gttgctaaaa tggataagct caatggttct 300
 gcgcgtctta tgattgtttc agacctcgat catacaatgg ttgatcatca tgacgaagag 360
 aacttgtcgt tgcttaggtt tggggccctt tggcgatctg cttactgtca gattctcta 420
 cttgtcttct cgaccggaag atcaccact ctctataagg aattgaggaa agagaagcct 480
 atgctaactc cagacatcac tattatgtcg gtgggcagtg agataactta tggtagggcc 540
 atggttcctg atgatggctg ggaggaatat ctgaacaata agtgggacag aaatattgtt 600
 cttgaggaga ccgctaagta ttctgagctg aagcttcagc cagagacaga acagcgtcca 660
 cataaggctc acttcttggg tgacaagaag agtgctcagg aagtataaaa gtctctctct 720
 gagaagtttg agaaacgtgg ggtagatgca aaaataatct atagtgggtg ccaagacctt 780
 gacatattag ctcaaggggc tggaaagggt caggcgcttg catatttact caagaagttc 840
 gcctcatgcg ggaacacacc caacaatact cttgtttgtg gtgactctgg caatgatgca 900
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<210> 130

<211> 3633

<212> DNA

<213> Festuca arundinacea

<400> 130

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<210> 131

<211> 3747

<212> DNA

<213> *Lolium perenne*

<400> 131

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<210> 132

<211> 3743

<212> DNA

<213> *Lolium perenne*

<400> 132

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<210> 133

<211> 2714

<212> DNA

<213> Lolium perenne

<400> 133

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<210> 134

<211> 2957

<212> DNA

<213> *Lolium perenne*

<400> 134

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<210> 135

<211> 1986

<212> DNA

<213> Festuca arundinacea

<400> 135

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<210> 136

<211> 2073

<212> DNA

<213> Lolium perenne

<400> 136

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<210> 137

<211> 1888

<212> DNA

<213> Festuca arundinacea

<400> 137

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<210> 138

<211> 1849

<212> DNA

<213> Lolium perenne

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<400> 138
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<210> 139

<211> 2166

<212> DNA

<213> *Lolium perenne*

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<210> 140

<211> 2137

<212> DNA

<213> Lolium perenne

<400> 140

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<210> 141

<211> 1954

<212> DNA

<213> Lolium perenne

<400> 141

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<210> 142

<211> 2039

<212> DNA

<213> *Lolium perenne*

<400> 142

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<210> 143

<211> 2006

<212> DNA

<213> *Lolium perenne*

<400> 143

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<210> 144

<211> 1789

<212> DNA

<213> *Lolium perenne*

<400> 144

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<210> 145

<211> 1358

<212> DNA

<213> Lolium perenne

<400> 145

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gccaccggcc	acctctcccc	gtacacgtac	aacctcagga	ggacgggccc	tgaagatgtg	180
gtgctgaagg	ttctgtactg	cggcatctgc	cacactgacc	tccaccagac	caagaaccac	240
cttggtgctt	caaaaataccc	catggttccc	gggcatgagg	tggtaggcga	ggtggtggag	300
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aagtggtgca	agtcctatgg	ccaccacgtc	accgtgatca	gctcctccga	caagaagcgc	720
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<210> 146

<211> 1051

<212> DNA

<213> Lolium perenne

<400> 146

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ccacggcgcc	tgatgccacg	gccacgggtg	ccaaggagca	gaccaccacc	aacggcgccg	120
ccagcggtgc	cgagcaggtc	acccgccact	ccgaggtcgg	gcacaagagc	ctgctccaga	180
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agaaggccgg	cgtcgcgcac	aagatcgact	tcgcgcgagg	gcccgcgctc	ccggtgctcg	540
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acaaggacaa	ctacctcaac	taccaccagc	gcctcatgaa	gctcgtcagg	gtcggcgggc	660
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ccatgggatgc	ggacaagaat	tgattaatta	ttattcccca	ttttgccgtt	ctggcctttct	960
tctgtatctt	cttggaataa	aatattgtcc	ctttatgtac	gtatatcaaa	tttatatcca	1020
gacaaataat	attactccta	taaaaaaaaa	a			1051

<210> 147

<211> 1332

<212> DNA

<213> *Lolium perenne*

<400> 147

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aacaccgcgt	ccatattaac	tatcaacatg	acagtcgtcg	aggtcttagc	tgccggcgac	180
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aagggcaccg	tcaggaaccc	agacgacccg	aagaacgcgc	acctgagggc	gctcgacggc	360
gccgccgacc	ggctggtcct	ctgcaaggcc	gacctcctcg	actacgacgc	catccgccgc	420
gccatcgacg	gctgccacgg	cgtcttccac	accgcatccc	cagtcactga	cgaccccgag	480
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gtaaaaaaaaa	aa					1332

<210> 148

<211> 1236

<212> DNA

<213> *Festuca arundinacea*

<400> 148

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gcctggccat	gggcagaccg	tgtgcgtcac	cgccgcgcgc	gggtacatcg	cgctggggct	180
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aagcaaacca	gagggattaa	acggtgtaac	ggcatgatac	tgctaaagaa	gcagcagagt	1140
tcacgtgctc	ctgtaacatg	gtcaaacatg	agttgttttt	ctgtataaat	tctatccagt	1200
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<210> 149

<211> 1428

<212> DNA

<213> *Festuca arundinacea*

<400> 149

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cgctgaagaa	gcctatcgag	cttggcctcc	tggagatcct	ggtggccgcc	ggcggcaagt	180
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<210> 150

<211> 1455

<212> DNA

<213> *Lolium perenne*

<400> 150

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<210> 151

<211> 2101

<212> DNA

<213> *Lolium perenne*

<400> 151
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<213> *Lolium perenne*

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<210> 153

<211> 2595

<212> DNA

<213> Festuca arundinacea

<400> 153

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<210> 154

<211> 1382

<212> DNA

<213> *Lolium perenne*

<400> 154

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<210> 155

<211> 1260

<212> DNA

<213> *Lolium perenne*

<400> 155

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<210> 156
 <211> 1204
 <212> DNA
 <213> *Lolium perenne*

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<210> 157
 <211> 1530
 <212> DNA
 <213> *Lolium perenne*

<400> 157
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<210> 158
 <211> 1418
 <212> DNA
 <213> *Festuca arundinacea*

<400> 158

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agaagggcct	gattccgctc	ggagcggaa	gggcaggcgg	cccggccagt	gcagccggca	1140
agctgggagc	tggtctcgtg	ggcgaagggtc	aggcgattgg	tgctgagaca	taagcgctag	1200
tgcattgtaca	ctaggtctggc	tacctcagac	acatgggtgga	gcgatgatta	tggttcgttaa	1260
ttctactatc	ctatatcttcg	gttcagaaat	tgcatataaga	gaaccctgta	attggtggga	1320
tattatgaac	ggattatgga	acgcaaataa	cttcatgaca	aaaaaaaaaa	aaaaaaaaaa	1380
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1418

<210> 159

<211> 1209

<212> DNA

<213> *Lolium perenne*

<400> 159

gagcaccaca	catggcgact	gaagccaagg	gggagacggg	gctgggtcacc	ggcgccagcg	60
gcttcatcgg	ctcctggctc	gtccgcctcc	tcctcgccc	cggctactcc	gtccacgccc	120
ccgtcctcaa	ccccgatgac	aaggccgaga	cggaccacct	cctcgcgctc	gccgctgcgg	180
ccggcgacga	gggcccgcac	cgcttcttca	gggtgcgacct	cctcgacggc	gccgccatgc	240
tcgcccgcgt	gcggggatgc	tccggcggtg	tccacctcgc	ctctccctgc	accgtcgacc	300
tcgtcctoga	ccccagaag	gagcttgtgg	tgccggcggt	ggaggggcacg	ctcaacgtgc	360
tgcgcgccgc	caagggaagct	gggggagtg	ggcggggtgg	ggtgacctcc	tccgtctccg	420
ccctcgctcc	ctgcccgggg	tggccggccg	gcgaggtcct	cgacgagcgc	tgctggaccg	480
acatcgacta	ctgcgacaag	aacgggggtt	ggtaccctgc	ttcaaaggca	ctggcggaga	540
aggcggcatg	gaagtttgca	gaggagaatg	gactggatgt	ggtgacggtc	aatccaggga	600
cgttttttgg	cgagatgatt	ccgccaaggc	tcaatgccag	catggccatg	tttcttcgct	660
tacttgaagg	ttgcaaagag	gagtatgcag	atttcttcat	cgggccagtg	cacgtggaag	720
acgttgcat	agcccatatt	ctgctgtacg	agaatccgtc	agcatccggg	aggcacctct	780
gcgtggagcc	catctgtcac	tggagtgttt	tccggcgcaa	agtcgcccag	ctctaccctg	840
attacaaagt	tccaaaattc	cctgaggaca	cacagcctgg	gctgggtgag	gcggagccgg	900
tgccaaagaa	gctgatggcg	ttgggtttgc	agttcactcc	tcttgagaag	atcatcaggg	960
atgccgtgga	gagcctcaag	agcagaggat	gcacgcctg	atgattggat	cgttaggcat	1020
gtcacccttc	cgtcgtagg	tcatgatcat	ccttggttag	agatgtgttg	tggtgtgtcc	1080
agcccagtg	ctaccagac	catatactta	ccagtatgat	ttgtgcaata	acagccgggt	1140
gatgtacggc	atcacctg	ctacacttgg	gatgcggatg	ctgtcacact	gactccctca	1200
aaaaaaaaaa						1209

<210> 160

<211> 1260

<212> DNA

<213> *Lolium perenne*

<400> 160

gaaaagcttc	acacagcttg	agaaaatggg	gagctcaacc	aaggggcaaag	tgtgtgtaac	60
tggggcttca	ggctttgttg	cctcttggct	catcaagaaa	ctccttgagt	ctggatatca	120
tgtgataggg	actgtcagag	acccagggaa	tcgaagaaag	gtgggacacc	tttggaact	180
accagggtgca	aatgagaggc	tccaacttgt	gagagctgat	ctattggagg	aaggggagctt	240
tgacgatgct	gtaagggctt	gtgaggggtg	cttccacatt	gcgtcgccctg	tccttgggaa	300
atctgattcc	aattgcaagg	aagcaacact	cggtcctgca	atcaatggta	ccctcaacgt	360

gctaagatcc	tgcaagaaga	gtccattttct	caaaaggggtt	gttctcacat	cttcatcatc	420
cgcggttaagg	attaggggatg	aaactcagca	gccagaactg	ttatgggatg	aaacgacatg	480
gagctctgtg	ccactctgtg	aaaagctaca	gctatggat	gccctggcaa	aggatatttcg	540
agagaaagca	gcattggact	ttgccaagga	gaataacatt	gaccttggtga	cagttcttcc	600
atcattcgta	attggaccca	gtttatccca	tgaattgtgc	actactgctt	cagatatcct	660
tggcttactt	caaggtgaca	cagacagggtt	cactttgtac	ggaaggatgg	gatatgttca	720
catcgatgat	gttggccgga	gccacattct	agtgtacgaa	acaccggagg	caactggcag	780
atatctgtgc	agctcagtg	ttctggataa	caatgaattg	gttggcttac	tggcaaaaca	840
gtttccagta	ttccccattc	caaggaggct	caagaacccc	tatggaaagc	aggcatacca	900
gctagacaca	tccaagctcc	aggggctggg	tctcaagttc	aaaggagtgc	aggagatgtt	960
taacgactgc	gtcgaatcgc	tgaaagatca	ggggcatttg	ctggagtgcc	cgttgtgata	1020
acagagacag	cattgacaag	ccatagccaa	acagcattga	caagccatag	ccaaacacat	1080
ctcaactatg	cctgaatcat	ctcagttctc	gagtcataga	tttttttttt	ctcttcaaat	1140
aattcccatg	tactctcctt	actataccga	acatcaattg	tcagcggcag	attaaatgtg	1200
tccatattgt	ttgcaattgt	ttcaattagt	aatgaaatat	ttgaaacaaa	aaaaaaaaaa	1260

<210> 161

<211> 1438

<212> DNA

<213> Lolium perenne

<400> 161

aaacgactcc	aacgcaccga	tcgacgacac	accctgcact	tcacgggtcg	atcggatcgg	60
aggatggcgc	cggtggtgga	gagagcgccc	ttcctgccga	cgggggaggc	cacgctgcgg	120
ccgtccttcg	tgcgggacga	ggacgagcgg	cccaagggtg	cgacgaccg	cttcagcgac	180
gaggtgcccg	tcatctcgct	ccacggcatc	gacgacgcgc	ggaggaccga	gatccgggac	240
cgctggtcgg	cggtgtgcga	gggtgtgggc	atcttccagg	tcgtcgacca	cggtcgtcag	300
gccgcgtca	tcgccgagat	ggccaggctc	tcgcgcgact	tcttcgcgct	ccccgcgag	360
gacaagctcc	gctacgacat	gtccggcggc	aagaaggcg	gattcatcgt	ctccagccac	420
ctccaggcgg	agacggtcca	ggactggcgg	gagatcgtga	cctacttctc	gtaccgggtc	480
aaggcgcggg	actacggccg	gtggccggac	aagcccgcgg	ggtggcgcg	ggtgggtggg	540
cagtacagcg	agcggctcat	ggcgtgtccc	tgcaagctgc	tgggggtgct	gtcggaggcc	600
atgggcctgg	agacggaggc	cctgtccaag	gcgtgcgtgg	acatggacca	gaagggtggtg	660
gtcaacttct	acccaagtg	ccccagccc	gacctacccc	tcggcctcaa	gcgccacacc	720
gaccccgga	ccatcacctc	cctcctccag	gacctcgtcg	gcggactcca	ggccaccgcg	780
gacggcgga	acacctggat	caccgtacag	cccatcgccg	gcgattcgt	cgtcaacctc	840
ggcgaccacg	gccactactt	gagcaacggg	aggtttaaga	acggggacca	ccaggcggtg	900
gtgaacgggg	agagcagcag	gctgtccatc	gccacgttcc	agaacccggc	gcccagcgcc	960
aagggtgtgg	cgctggcggt	gagggagggg	gaggacacca	tcctggagga	gcccatacc	1020
ttcaccgaga	tgtaccgccg	caagatggcg	cgcgacctcg	agctogccaa	gcgcaagaag	1080
caggccaagg	ccgatcagct	caagcagcag	ctgcagcagg	aggccgcgcc	cgccgcgcg	1140
cccaccaagc	catcaacca	gattcttgcc	tagattccat	gccgattcat	tcactcgtga	1200
tatatagtac	tatgtactat	atcgtaataa	aataagtaat	tatctctatc	tactcatttg	1260
tgtgtaatta	agagatgagt	aattatctag	tatatacaca	tttgtctgcg	aggagcgagc	1320
tggacctgta	ataacatgta	gcatgtccta	cgtggaaccg	atcagctgat	tggagctgtc	1380
acatgagttt	gctgtgtgca	gaaattgaac	gcattcggta	ctgctttcaa	aaaaaaaa	1438

<210> 162

<211> 1214

<212> DNA

<213> Lolium perenne

<400> 162

gaaaatcccc	aaacccaaaa	ggtgaggcct	ccagatactt	ggatctccaa	tggctcctgc	60
tactcccaag	gacagctcta	gctctgctct	gcctgggtttg	ctcttgetcc	tcgcagcagc	120
gacgtccgtg	gcggtagcga	acgcacagct	atcagagaaac	tactacgggt	cttcttgtcc	180
caccgcgctt	cttccatca	ggactgtcgt	gacgacggcg	gtgctgctgg	accaccgcat	240
gggcgcttct	cttctccggc	tcacttcca	cgactgcttt	gtgcaagggt	gcgacgcgtc	300
cgttctgctg	gatgacacgg	ccggcttcac	cggcgagaag	ggggccgggc	cgaacgccgg	360
gtcgtcgcgc	ggtctggagg	tgatcgacaa	gatcaagatg	ctgctggagt	tcatgtgccc	420
gcggaaccgtc	tcctgcgcgc	acatcctcgc	cgtgcgcgcc	cgcgactccg	tcgtccgtct	480
aggggggcca	tcatggcgcg	ttcaacttgg	aaggagggac	gccaccacag	caagcgcgtc	540
acttgctagt	agtgacctcc	caggccccaa	ctccaaacctc	aatgatctcc	tcaccgcttt	600
ctccaaaaaa	ggactaagca	ccacggacat	ggttgctcta	tcaggggccc	ataccatcgg	660
ccgggcgcag	tgccagaact	accggaaccg	gatctacacc	gacaccgaca	ttgacggggc	720
attcgcagcg	tccctgcgag	gcggctgccc	acaggccggc	ggcgacggca	acctcgcgcc	780

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gctcgacgcg tcctctccca acaccttcga taacggctac ttctccggcc tcctctcccg 840
ccaggggctg ctccattccg accaggcgct gtacgacggc ggctccacgg acgatctggg 900
caggacctac gcctccaata acgatcagtt tggcagcgac ttcgctgcgg cgatggtgaa 960
actgagcaat atcggcctgc tgacgggggc gtccggggag atcagggtca actgccgggc 1020
ggtgaattaa cgatggatgg atgggggcat catgaaacga acaaggcgtg cgatttccgg 1080
aactgcaggc aacgaaactg catatttatg tacactgcct atttatttcc tgccttgtg 1140
tccccgtctt gttatattac atccataatc catgttaaga tgggtggcatt ggtttaaaaa 1200
aaaaaaaaaa aaaa 1214

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<210> 163

<211> 654

<212> PRT

<213> *Lolium perenne*

<400> 163

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Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Pro Leu Leu Pro
1      5      10      15
Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ser Asp Asp Ala Arg Glu Asn
20     25     30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
35     40     45
Ala Ser Ala Leu Ala Val Val Val Val Gly Leu Leu Ala Gly Gly
50     55     60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65     70     75     80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85     90     95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100    105    110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115    120    125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130    135    140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145    150    155    160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165    170    175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180    185    190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195    200    205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210    215    220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225    230    235    240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys
245    250    255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260    265    270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275    280    285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290    295    300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305    310    315    320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325    330    335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340    345    350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355    360    365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370    375    380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385    390    395    400

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Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
      405      410      415
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
      420      425      430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
      435      440      445
Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
      450      455      460
Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
      465      470      475      480
Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
      485      490      495
Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
      500      505      510
Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
      515      520      525
Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
      530      535      540
Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
      545      550      555      560
Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
      565      570      575
Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
      580      585      590
Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
      595      600      605
Tyr Pro Thr Glu Ala Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
      610      615      620
Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
      625      630      635      640
Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
      645      650

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<210> 164

<211> 620

<212> PRT

<213> Festuca arundinacea

<400> 164

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Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
  1      5      10      15
Pro Thr Ala Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
  20      25      30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
  35      40      45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
  50      55      60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
  65      70      75      80
Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
  85      90      95
Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
  100      105      110
Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
  115      120      125
Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
  130      135      140
Pro Leu Ala Leu Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
  145      150      155      160
Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
  165      170      175
Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
  180      185      190
Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
  195      200      205

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Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp Ala Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
 260 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415
 Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Asp Asn Gly Ser Val
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Arg Gly Ala Ile
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Thr Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu His Gly Glu
 530 535 540
 Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
 610 615 620

<210> 165

<211> 623

<212> PRT

<213> Festuca arundinacea

<400> 165

Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45

Leu Leu Val Gly Ala Thr Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
 65 70 75 80
 Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
 85 90 95
 Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
 100 105 110
 Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
 115 120 125
 Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
 130 135 140
 Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
 145 150 155 160
 Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
 165 170 175
 Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
 180 185 190
 Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
 195 200 205
 Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
 210 215 220
 Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
 225 230 235 240
 Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
 245 250 255
 His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
 260 265 270
 Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
 275 280 285
 Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
 435 440 445
 Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
 450 455 460
 Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
 465 470 475 480
 Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
 485 490 495
 Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
 500 505 510
 Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
 515 520 525
 Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
 530 535 540
 Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
 545 550 555 560
 Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
 565 570 575

Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
 580 585 590
 Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
 595 600 605
 Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
 610 615 620

<210> 166

<211> 619

<212> PRT

<213> Festuca arundinacea

<400> 166

Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
 65 70 75 80
 Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
 85 90 95
 Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
 100 105 110
 Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
 115 120 125
 Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
 130 135 140
 Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
 145 150 155 160
 Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
 165 170 175
 Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
 180 185 190
 Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
 195 200 205
 Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
 260 265 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415

Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Arg Gly Ala Leu
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
 530 535 540
 Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
 610 615

<210> 167

<211> 1075

<212> PRT

<213> Lolium perenne

<400> 167

Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp
 1 5 10 15
 Ala Gly Gly Thr Ala Gly Asp Ile Ser Ala Ala Ser Val Ala Gly Gly
 20 25 30
 Asp Asp Gly Pro Gly Ala Gly Gly Thr Ala Gly Glu Lys Arg Asp
 35 40 45
 Lys Ser Ser Leu Met Leu Arg Glu Arg Gly Arg Phe Asn Pro Ala Arg
 50 55 60
 Tyr Phe Val Glu Glu Val Ile Ser Gly Phe Asp Glu Thr Asp Leu Tyr
 65 70 75 80
 Lys Thr Trp Val Arg Thr Ser Ala Met Arg Ser Pro Gln Glu Arg Asn
 85 90 95
 Thr Arg Leu Glu Asn Met Ser Trp Arg Ile Trp Asn Leu Ala Arg Lys
 100 105 110
 Lys Lys Gln Ile Glu Gly Glu Glu Ala Ser Arg Leu Ser Lys Lys Arg
 115 120 125
 Leu Glu Arg Glu Lys Ala Arg Arg Asp Ala Ala Ala Asp Leu Ser Glu
 130 135 140
 Asp Leu Ser Glu Gly Glu Lys Gly Glu Asn Ile Asn Gly Ser Ser Val
 145 150 155 160
 His Asp Glu Ser Thr Arg Gly Arg Met Pro Arg Ile Gly Ser Thr Asp
 165 170 175
 Ala Ile Glu Val Trp Ala Asn Gln His Lys Asp Lys Lys Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Ile Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Gly Glu Thr Pro Gly Val Tyr Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Ala Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro
 245 250 255

Thr Glu Met Leu Ser Pro Arg Asn Ser Glu Asn Leu Gly Asp Asp Met
 260 265 270
 Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly Pro Arg
 275 280 285
 Glu Lys Tyr Ile Pro Lys Glu Gln Leu Trp Pro His Ile Gln Glu Phe
 290 295 300
 Val Asp Gly Ala Leu Val His Ile Met Gln Met Ser Lys Val Leu Gly
 305 310 315 320
 Glu Gln Val Gly Arg Glu Arg Arg Val Trp Pro Val Val Ile His Gly
 325 330 335
 His Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
 340 345 350
 Asn Val Pro Met Val Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu
 355 360 365
 Glu Gln Leu Leu Lys Gln Gly Arg Gln Thr Arg Asp Glu Val Asn Ala
 370 375 380
 Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Cys Leu Asp
 385 390 395 400
 Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Glu Lys Gln
 405 410 415
 Trp Gly Leu Tyr Asn Gly Phe Asp Val Thr Met Glu Arg Lys Leu Arg
 420 425 430
 Ala Arg Thr Lys Arg Gly Val Ser Cys Tyr Gly Arg Tyr Met Pro Arg
 435 440 445
 Met Ile Ala Ile Pro Pro Gly Met Glu Phe Ser His Ile Val Pro His
 450 455 460
 Asp Val Asp Leu Asp Gly Asp Glu Ala Asn Glu Val Gly Ser Gly Ser
 465 470 475 480
 Pro Asp Pro Pro Ile Trp Ala Asp Ile Met Arg Phe Phe Ser Asn Pro
 485 490 495
 Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn
 500 505 510
 Ile Thr Thr Leu Val Lys Ala Phe Gly Glu His Pro Gly Leu Arg Asn
 515 520 525
 Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Val Ile Asp Glu
 530 535 540
 Met Ser Ser Thr Asn Gly Ala Val Leu Thr Ser Val Leu Lys Leu Ile
 545 550 555 560
 Asp Lys Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
 565 570 575
 Gln Ser Glu Val Pro Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys Gly
 580 585 590
 Val Phe Ile Asn Cys Ala Tyr Ile Glu Pro Phe Gly Leu Thr Leu Ile
 595 600 605
 Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Gln Asn Gly Gly
 610 615 620
 Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Ile Leu Val Asp Pro
 625 630 635 640
 His Asn Gln Asn Asp Ile Ala Glu Ala Leu Tyr Lys Leu Val Ser Asp
 645 650 655
 Lys His Leu Trp Ala Gln Cys Arg Gln Asn Gly Leu Asp Asn Ile His
 660 665 670
 Arg Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Val Gly
 675 680 685
 Thr Val Lys Pro Arg His Pro Arg Trp Gln Arg Ser Asp Asp Ala Thr
 690 695 700
 Glu Val Ser Glu Ser Asp Ser Pro Gly Asp Ser Leu Arg Asp Val His
 705 710 715 720
 Asp Ile Ser Leu Asn Leu Lys Leu Ser Leu Asp Ser Glu Lys Ala Gly
 725 730 735
 Thr Lys Ile Asn Thr Glu Arg Asn Ser Thr Asn Ala Arg Arg Asn Leu
 740 745 750
 Glu Asp Ala Val Leu Lys Phe Ser Asn Ala Val Ser Glu Gly Thr Lys
 755 760 765
 Asp Glu Ser Asp Glu Asn Ala Glu Ala Thr Thr Gly Ser Asn Lys Trp
 770 775 780

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<210> 168
<211> 938
<212> PRT
<213> Lolium perenne
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<400> 168

Met 1	Ala	Ala	Gly	Asn 5	Glu	Trp	Ile	Asn	Gly 10	Tyr	Leu	Glu	Ala	Ile 15	Leu
Asp	Ala	Gly	Ser 20	Lys	Leu	Arg	Pro	Gln 25	Gly	Val	Gln	Leu	Pro 30	Pro	Leu
Glu	Thr	Ala 35	Pro	Ala	Leu	Ala	Ala 40	Glu	Glu	Ser	Ser	Ala 45	Ala	Tyr	Asn
Pro	Thr 50	Arg	Tyr	Phe	Val	Glu 55	Glu	Val	Val	Arg	Ser 60	Phe	Asp	Glu	Gln
Ala 65	Leu	His	Lys	Thr	Trp 70	Thr	Lys	Val	Val	Ala 75	Met	Arg	Asn	Ser	Gln 80
Glu	Arg	Ser	Asn 85	Arg	Leu	Glu	Asn	Leu	Cys 90	Trp	Arg	Ile	Trp 95	Asn	Val
Ser	Arg	Gln	Lys 100	Lys	Gln	Val	Glu	Trp 105	Asp	Tyr	Thr	Lys	Glu 110	Val	Ala
Arg	Arg	Lys 115	Leu	Glu	Gln	Glu	Leu 120	Gly	Ser	Arg	Glu	Ala 125	Ala	Glu	Asp
Leu	Ser 130	Glu	Leu	Ser	Glu	Gly 135	Glu	Lys	Asp	Thr	Thr 140	Thr	Ala	Lys	Pro
Asp 145	Ala	Ala	Ala	Ala 150	Gln	Pro	Ser	Ala	Asp 155	Asp	Gly	Glu	His	Gln	Gln 160

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Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
      165      170      175
Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
      180      185      190
Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
      195      200      205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
      210      215      220
Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
      225      230      235
Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
      245      250      255
Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp
      260      265      270
Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
      275      280      285
Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
      290      295      300
Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
      305      310      315
Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
      325      330      335
Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
      340      345      350
Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
      355      360      365
Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
      370      375      380
Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr Tyr Lys Ile Ala
      385      390      395
Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr Ala Glu Met Val
      405      410      415
Val Thr Ser Thr Lys Gln Glu Ile Glu Gln Trp Gly Leu Tyr Asp
      420      425      430
Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val Arg Gln Arg Arg
      435      440      445
Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met Ala Val Ile Pro
      450      455      460
Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp Thr Ala Asp Gly
      465      470      475
Asp Gly Ala Asp Leu Gln Met Leu Ile Ala Pro Asp Lys Ala Lys Lys
      485      490      495
Ala Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe Phe Thr Asn Pro
      500      505      510
His Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp Pro Lys Lys Asn
      515      520      525
Val Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg Gln Leu Arg Glu
      530      535      540
Leu Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp Asp Ile Glu Asp
      545      550      555
Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val Leu Lys Leu Ile
      565      570      575
Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
      580      585      590
Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly
      595      600      605
Val Phe Ile Asn Pro Ala Leu Val Glu Pro Phe Gly Leu Thr Ile Ile
      610      615      620
Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr Lys Asn Gly Gly
      625      630      635
Pro Val Asp Ile Leu Lys Ala Leu His Asn Gly Leu Leu Val Asp Pro
      645      650      655
His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser Leu Leu Ala Glu
      660      665      670
Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu Arg Asn Ile His
      675      680      685

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Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu Ser His Val Ser
690 695 700
Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu Arg Val Pro Leu
705 710 715 720
Ala Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp Ser Leu Ser Asp
725 730 735
Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp Ala Ser Ser Asp
740 745 750
Leu Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp Ala Leu Arg Arg
755 760 765
Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala Arg Ala Leu Gly
770 775 780
Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val Ala Val Asp Cys
785 790 795 800
Tyr Gly Asp Asp Gly Lys Pro Asp Val Glu Gln Leu Lys Lys Ala Ile
805 810 815
Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala Lys Gln Gly Tyr
820 825 830
Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala Glu Ala Ile Lys
835 840 845
Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu Ile Cys Ser Ser
850 855 860
Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Val Ala Asp Glu Glu
865 870 875 880
Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp His Val Lys Ser
885 890 895
Ala Val Pro Arg Leu Gly Ser Met Glu Glu Ile Ala Leu Ala Ile Asp
900 905 910
Arg Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala
915 920 925
Ser Lys Val Ser Ile Thr Glu His Tyr Leu
930 935

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<210> 169

<211> 808

<212> PRT

<213> Lolium perenne

<400> 169

```

Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
1 5 10 15
Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
35 40 45
Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
50 55 60
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
85 90 95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
100 105 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
115 120 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
130 135 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145 150 155 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
165 170 175
Asn Phe Leu Lys Ala His Asn His Lys Gly Thr Thr Met Met Leu Asn
180 185 190
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
195 200 205

```

Glu Glu Tyr Leu Thr Ser Ile Pro Glu Asp Thr Pro Ser Ser Glu Phe
 210 215 220
 Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
 225 230 235 240
 Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Leu Asp Leu Leu Glu
 245 250 255
 Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
 260 265 270
 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
 275 280 285
 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
 290 295 300
 Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
 305 310 315 320
 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
 325 330 335
 Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
 340 345 350
 Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
 355 360 365
 Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
 370 375 380
 Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
 385 390 395 400
 Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
 405 410 415
 Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
 420 425 430
 His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
 435 440 445
 Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
 450 455 460
 Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
 465 470 475 480
 Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
 485 490 495
 Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
 500 505 510
 Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Thr Val Tyr
 515 520 525
 Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
 530 535 540
 Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
 545 550 555 560
 Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
 565 570 575
 Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
 580 585 590
 Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
 595 600 605
 Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
 610 615 620
 Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Glu Gly His Ile Arg Trp Ile
 625 630 635 640
 Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
 645 650 655
 Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
 660 665 670
 Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
 675 680 685
 Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asn Gly Val Ser Gly
 690 695 700
 Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
 705 710 715 720
 Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
 725 730 735

Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
 770 775 780
 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Val Pro Leu Ala
 785 790 795 800
 Val Asp Gly Glu Asn Thr Asp Asn
 805

<210> 170

<211> 815

<212> PRT

<213> Lolium perenne

<400> 170

Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
 20 25 30
 Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
 130 135 140
 Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
 145 150 155 160
 Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
 165 170 175
 Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
 180 185 190
 Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
 195 200 205
 Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
 210 215 220
 Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
 225 230 235 240
 Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
 245 250 255
 Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
 260 265 270
 Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
 275 280 285
 His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
 290 295 300
 Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
 305 310 315 320
 Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
 325 330 335
 Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
 340 345 350
 Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
 355 360 365
 Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
 370 375 380
 Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His

```

385          390          395          400
Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
405
Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
420
Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
435
Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
450
Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
465
Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
485
Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
500
Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
515
Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
530
Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Asp Val
545
Asp Asn Asp Glu His Lys Phe Val Leu Lys Asp Arg Asn Lys Pro Ile
565
Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu
580
Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu
595
Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu
610
Gln Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu
625
Asn Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn
645
Ala Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln
660
Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr
675
Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile
690
Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp
705
Lys Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp
725
His Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu
740
Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr
755
Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu
770
Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met
785
Ala Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
805

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<210> 171

<211> 581

<212> PRT

<213> Festuca arundinacea

<400> 171

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Met Ala Gln Ala Trp Ala Phe Phe Leu Leu Ala Leu Phe Ser Phe Ser
1          5          10          15
Ser Tyr Val Ser Arg Ile Phe Leu Cys Ser Arg Asn Gly Glu Gly Ser
20          25          30
Phe Leu Cys Ala Arg Ala Pro Glu Val Pro Ser Ile Ala Ser Asp Arg
35          40          45

```

Tyr Arg Thr Ala Tyr His Phe Gln Pro His Lys Asn Trp Met Asn Asp
 50 55 60
 Pro Asn Gly Pro Met Tyr Tyr Asn Gly Ile Tyr His Leu Phe Phe Gln
 65 70 75 80
 His Asn Pro Asn Gly Pro Gln Trp Gly Asp Ile Val Trp Gly His Ser
 85 90 95
 Val Ser Thr Asp Leu Val Asn Trp Ile Ile Leu Glu Pro Ala Ile Glu
 100 105 110
 Pro Asp Thr Pro Gly Asp Ile Lys Gly Cys Trp Ser Gly Ser Ala Thr
 115 120 125
 Val Ile Ser Gly Ser Gln Pro Val Ile Met Tyr Thr Gly Gly Asp Val
 130 135 140
 Glu Asn His Gln Val Gln Asn Ile Ala Leu Pro Lys Asn Arg Ser Asp
 145 150 155 160
 Pro Tyr Leu Ile Glu Trp Thr Lys Ala Cys Asn Asn Pro Val Leu Gln
 165 170 175
 Pro Val Gly Pro Gly Met Asn Pro Gly Glu Phe Arg Asp Pro Thr Thr
 180 185 190
 Gly Trp Ile Gly Pro Asp Gly Leu Trp Arg Ile Ser Ile Gly Ala Glu
 195 200 205
 Val Asn Gly Tyr Ser Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu
 210 215 220
 Asn Trp Ser Arg Val Asp His Pro Leu Tyr Ser Ser Ser Ala Ser Thr
 225 230 235 240
 Met Trp Glu Cys Leu Asp Phe Phe Ala Val Leu Pro Gly Ser Asn Gly
 245 250 255
 Gly Leu Asp Leu Ser Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu
 260 265 270
 Lys Val Ser Val Asp Gln Cys Asp Lys Tyr Met Ile Gly Val Tyr Asp
 275 280 285
 Leu Glu His Asp Ala Phe Val Pro Asp Thr Ile Leu Asp Asp Arg Trp
 290 295 300
 Leu Leu Pro Arg Ile Asp Tyr Gly Asn Tyr Tyr Ala Ser Lys Ser Phe
 305 310 315 320
 Phe Asp Ser Lys Asn Arg Arg Arg Ile Ile Trp Gly Trp Thr Asn Glu
 325 330 335
 Ser Asp Ser Ser Asp Asp Val Ala Lys Gly Trp Ala Gly Ile Tyr
 340 345 350
 Ala Ile Pro Arg Thr Ile Trp Leu Asp Arg Asp Gly Lys Gln Leu Leu
 355 360 365
 Gln Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Arg Asn Glu Ile Asn
 370 375 380
 Tyr Gln Gly Leu Asp Leu Glu Lys Gly Asp Leu Tyr Glu Ile Lys Gly
 385 390 395 400
 Val Asp Thr Leu Gln Ala Asp Val Glu Ile Asp Phe Glu Leu Thr Ser
 405 410 415
 Ile Asp Asp Ala Asp Ser Phe Asp Pro Ser Trp Leu Leu Asp Pro Glu
 420 425 430
 Lys His Cys Arg Glu Ala Gly Ala Ser Val His Gly Gly Ile Gly Pro
 435 440 445
 Phe Gly Leu Val Ile Leu Ala Thr Gly Asp Met Glu Glu His Thr Val
 450 455 460
 Val His Phe Arg Val Tyr Lys Ser Gln Lys Glu Tyr Met Ile Leu Met
 465 470 475 480
 Cys Ser Asp Ile Arg Arg Ser Ser Leu Arg Gln Gly Leu Tyr Ala Pro
 485 490 495
 Ala Tyr Gly Gly Phe Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile
 500 505 510
 Ser Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly
 515 520 525
 Gly Gly Arg Val Cys Ile Ile Ala Arg Val Tyr Pro Val Ala Ile Val
 530 535 540
 Asp Asp Gly Ser Ala His Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr
 545 550 555 560

Val Arg Val Pro Gln Ile Arg Ala Trp Ser Met Met Thr Ala Gln Val
 565 570 575
 Asn Leu Lys Lys Gly
 580

<210> 172
 <211> 562
 <212> PRT
 <213> Lolium perenne

<400> 172
 Met Asn Gly Ile Glu His Pro Gly Asn Gly Arg Thr Ala Tyr His Phe
 1 5 10 15
 Gln Pro Ala Lys His Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
 20 25 30
 Asn Gly Leu Tyr His Phe Phe Tyr Gln Tyr Asn Pro His Gly Pro Thr
 35 40 45
 Trp Asp Thr Gly Lys Leu Ser Trp Gly His Ser Val Ser Gly Asp Leu
 50 55 60
 Val Asn Trp Ala Ala Leu Asp Asn Ala Leu Asp Pro Thr Ala Pro Phe
 65 70 75 80
 Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Gly Gly
 85 90 95
 Arg Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Asp Lys Val Gln Val
 100 105 110
 Gln Asn Val Ala Phe Ala Lys Asp Pro Ser Asp Pro Leu Leu Arg Glu
 115 120 125
 Trp Glu Lys Pro Ser Cys Asn Pro Val Ile Pro Tyr Pro Ala Asp Val
 130 135 140
 Thr Gly Asn Asn Phe Arg Asp Pro Thr Glu Ala Trp Arg Gly Arg Asp
 145 150 155 160
 Gly Leu Trp Arg Val Gly Ile Val Ala Glu Val Lys Gly Val Gly Ser
 165 170 175
 Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp Gln Arg Asn Ala
 180 185 190
 Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val Leu Glu Cys Pro
 195 200 205
 Asp Leu Phe Pro Val Ala Ala Ala Gln Gly Ala Thr Glu Gly Leu
 210 215 220
 Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His Val Leu Lys Leu
 225 230 235 240
 Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly Phe Tyr Asp Asp
 245 250 255
 Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg Gly Asp Asp Pro
 260 265 270
 Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr Ala Ser Lys Ser
 275 280 285
 Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp Ala Trp Val Asp
 290 295 300
 Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala Gly Ile Gln Ala
 305 310 315 320
 Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys Arg Leu Val Gln
 325 330 335
 Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys Arg Val Gly Leu
 340 345 350
 Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys Glu Ile Ala Gly
 355 360 365
 Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe Glu Ile Pro Asn
 370 375 380
 Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val Leu Asp Pro Lys
 385 390 395 400
 Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly Gly Val Gly Pro
 405 410 415
 Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu Glu His Thr Ala
 420 425 430
 Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr Lys Val Leu Met

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<210> 173
<211> 580
<212> PRT
<213> Festuca arundinacea
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Met 1	Ala	His	Ala	Trp 5	Ala	Phe	Phe	Leu	Leu 10	Ala	Leu	Phe	Ser	Phe 15	Ser
Ser	Cys	Val	Ser	Lys 20	Leu	Phe	Ile	Tyr 25	Ser	Arg	Asn	Gly	Glu 30	Gly	Ser
Phe	Leu	Cys 35	Thr	Arg	Ser	Pro	Glu 40	Val	Pro	Ser	Ile	Ala 45	Ser	Lys	Arg
Tyr	Arg	Thr	Ala	Tyr	His	Phe 55	Gln	Ser	Pro	Lys	Asn 60	Trp	Ile	Asn	Asp
Pro 65	Cys	Gly	Pro	Met	Tyr 70	Tyr	Asn	Gly	Ile	Tyr 75	His	Glu	Phe	Tyr	Gln 80
Tyr	Asn	Pro	Gly	Gly 85	Thr	Ile	Ala	Ala	Asn 90	Ile	Val	Trp	Gly	His 95	Ser
Val	Ser	Thr	Asp 100	Leu	Val	Asn	Trp	Ile 105	Gln	Leu	Glu	Pro	Ala 110	Ile	Val
Arg	Asp	Thr	Pro 115	Tyr	Asp	Ile	His 120	Gly	Cys	Trp	Thr	Gly 125	Ser	Ile	Thr
Ile	Leu 130	Pro	Gly	Asp	Gln	Pro 135	Val	Ile	Ile	Tyr 140	Thr	Gly	Arg	Asp	Ser
Asp 145	Asn	His	Gln	Ser	Gln 150	Asn	Ile	Glu	Leu 155	Pro	Lys	Asn	Arg	Ser	Asp 160
Pro	Tyr	Leu	Arg 165	Glu	Trp	Thr	Lys	Ala 170	Asp	Asn	Asn	Pro	Arg	Ile 175	Leu
Pro	Val	Gly	Pro 180	Asp	Leu	Asn	Leu 185	Thr	Gln	Phe	Arg	Asp	Pro 190	Thr	Thr
Gly	Trp	Ile 195	Gly	Pro	Asp	Gly	Leu 200	Trp	Arg	Ile	Ala 205	Ile	Gly	Ala	Glu
Leu	Asn 210	Gly	Tyr	Gly	Ala	Ala 215	Leu	Leu	Tyr	Lys 220	Ser	Glu	Asp	Phe	Leu
Asn 225	Trp	Thr	Arg	Val	Asp 230	His	Pro	Leu	Tyr	Ser 235	Asp	Asn	Ala	Pro	Ser 240
Met	Trp	Glu	Cys 245	Pro	Asp	Phe	Phe	Ala	Val 250	Leu	Pro	Gly	Asn	Asn 255	Gly
Gly	Leu	Asp 260	Leu	Ser	Ala	Ala	Ile	Pro 265	Lys	Gly	Ala	Lys	His 270	Val	Leu
Lys	Met 275	Ser	Val	Asp	Tyr	Ser	Asp 280	Lys	Tyr	Met	Ile	Gly 285	Val	Tyr	Asp
Leu	Lys 290	Arg	Asp	Ala	Phe	Val 295	Pro	Asp	Val	Val 300	Leu	Asp	Asp	Arg	Arg
Leu 305	Trp	Leu	Arg	Ile	Asp 310	Tyr	Gly	Thr	Phe 315	Tyr	Ala	Ser	Lys	Ser	Phe 320
Phe	Asp	Ser	Lys 325	Arg	Gly	Arg	Arg	Val	Ile 330	Trp	Gly	Trp	Ser	Asn 335	Glu

Thr Asp Ser Val Ser Asp Asp Gly Ala Lys Gly Trp Ala Gly Ile His
 340 345 350
 Ala Ile Pro Arg Ser Ile Trp Leu Asp Ser Asp Gly Lys Gln Leu Leu
 355 360 365
 Gln Trp Pro Ile Asp Glu Ile Glu Ser Leu Arg Arg Asp Glu Ile Asn
 370 375 380
 His Gln Gly Leu Glu Leu Lys Asn Gly Asp Leu Phe Glu Ile Lys Gly
 385 390 395 400
 Ile Asp Thr Leu Gln Ala Asp Ile Glu Val Asp Phe Glu Leu Thr Ser
 405 410 415
 Ile Asp Ser Ala Asp Pro Phe Asp Pro Ser Trp Leu Leu Asp Val Glu
 420 425 430
 Arg His Cys Arg Glu Ala Gly Ala Ser Val Gln Gly Gly Ile Gly Pro
 435 440 445
 Phe Gly Leu Val Val Leu Ala Ser Asp Asn Met Glu Glu His Ile Ala
 450 455 460
 Val His Phe Arg Val Tyr Lys Ser Gln Lys Ser His Met Ile Leu Met
 465 470 475 480
 Cys Ser Asp Leu Arg Arg Ser Ser Leu Arg Ser Gly Leu Tyr Thr Pro
 485 490 495
 Ala Tyr Gly Gly Phe Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile
 500 505 510
 Ser Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly
 515 520 525
 Gly Gly Arg Val Cys Ile Thr Ala Arg Ile Tyr Pro Val Ala Leu Val
 530 535 540
 Asp Gly Arg Val His Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val
 545 550 555 560
 Arg Val Pro Gln Leu Gly Ala Trp Ser Met Met Thr Ala Gln Val Asn
 565 570 575
 Val Asn Lys Gly
 580

<210> 174

<211> 569

<212> PRT

<213> Festuca arundinacea Lolium perenne

<400> 174

Met Ala Gln Gly Trp Pro Phe Phe Leu Leu Val Leu Phe Ser Ser Cys
 1 5 10 15
 Val Ser Asn His Leu Val Asn Gly Glu Arg Val Phe Leu Phe Pro Gln
 20 25 30
 Ser His Lys Val Ser Ser Ile Val Ser Lys Arg Tyr Arg Thr Ala Tyr
 35 40 45
 His Phe Gln Pro Pro Lys Asn Trp Ile Asn Gly Pro Met Tyr Tyr Asn
 50 55 60
 Gly Ile Tyr His Glu Phe Tyr Gln Tyr Asn Pro Asn Gly Ser Leu Trp
 65 70 75 80
 Gly Asn Ile Ile Trp Gly His Ser Val Ser Thr Asp Leu Ile Asn Trp
 85 90 95
 Ile Pro Val Glu Pro Ala Ile Glu Arg Asp Ile Pro Ser Asp Ile Asn
 100 105 110
 Gly Cys Trp Thr Gly Ser Ala Thr Ile Ile Ser Gly Asp Gln Pro Ile
 115 120 125
 Ile Ile Tyr Thr Gly Ala Asp Lys Glu Asn Arg Gln Leu Gln Asn Ile
 130 135 140
 Val Leu Pro Lys Asn Lys Ser Asp Pro Tyr Leu Arg Glu Trp Thr Lys
 145 150 155 160
 Ala Gly Asn Asn Pro Val Ile Gln Pro Val Gly Pro Gly Leu Asn Ala
 165 170 175
 Ser Gln Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro Asp Gly Leu
 180 185 190
 Trp Arg Ile Ala Val Gly Ala Glu Leu Asn Gly Tyr Gly Ala Ala Leu
 195 200 205
 Leu Tyr Lys Ser Gln Asp Phe Leu Asn Trp Thr Arg Val Asp His Pro

210	215	220
Leu Tyr Ser Ser Asn Ala Ser Ser Met Trp Glu Cys Pro Asp Phe Phe		
225	230	235
Ala Val Leu Pro Gly Asn Ser Gly Gly Leu Asp Leu Ser Ala Glu Ile		
	245	250
Pro Asn Gly Ala Lys His Val Leu Lys Met Ser Leu Asp Ser Cys Asp		
	260	265
Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Ser Asp Thr Phe Met Pro		
	275	280
Asp Ser Val Leu Asp Asp Arg Arg Leu Trp Ser Arg Ile Asp His Gly		
	290	295
Asn Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Lys Gly Arg Arg		
305	310	315
Ile Ile Trp Gly Trp Thr Asn Glu Thr Asp Ser Ser Ser Asp Asp Val		
	325	330
Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Thr Ile Trp Leu		
	340	345
Asp Ser Tyr Gly Lys Gln Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu		
	355	360
Ser Leu Arg Arg Asn Glu Ile Ser His Gln Gly Leu Glu Leu Lys Lys		
	370	375
Gly Asp Leu Phe Glu Ile Lys Gly Thr Asp Thr Ser Gln Ala Asp Val		
385	390	395
Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Asn Ala Asp Pro Phe Asp		
	405	410
Pro Ser Trp Leu Leu Asp Val Glu Lys Gln Cys Arg Glu Ala Gly Ala		
	420	425
Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val Leu Ala Ser		
	435	440
Asp Asn Met Glu Glu His Thr Ala Val His Phe Arg Val Tyr Lys Ser		
	450	455
Gln Gln Ser Tyr Met Ile Leu Met Cys Ser Asp Leu Arg Arg Ser Ser		
465	470	475
Leu Arg Ser Gly Met Tyr Thr Pro Ala Tyr Gly Gly Phe Phe Glu Phe		
	485	490
Asp Leu Gln Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp Arg		
	500	505
Ser Ala Val Glu Ser Phe Gly Gly Gly Arg Val Cys Ile Met Ala		
	515	520
Arg Val Tyr Pro Val Val Leu Val Asp Asp Gly Gly Ala His Met Tyr		
	530	535
Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu Arg Ala		
545	550	555
Trp Ser Met Ser Arg Ala Glu His Lys		
	565	

<210> 175

<211> 588

<212> PRT

<213> Lolium perenne

<400> 175

Met Gly Val Arg Leu Gly Arg Val Ala Trp Ala Cys Pro Ala Val Leu		
1	5	10
Val Leu Leu Leu Gln Leu Ala Gly Ala Ser His Val Val Tyr Glu Thr		
	20	25
Ser Leu Leu Glu Thr Glu Ala Ala Ala Thr Val Pro Ala Ser Ile		
	35	40
Phe Glu Leu Ser Thr Gly Tyr His Phe Arg Pro Gln Lys Asn Trp Ile		
	50	55
Asn Asp Pro Asn Ala Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe		
65	70	75
Phe Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Val Trp Ala		
	85	90
His Ser Val Ser Arg Asp Leu Ile Asn Trp Val Ala Leu Glu Thr Ala		
	100	105
		110

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Leu Ala Pro Ser Ile Asp Ala Asp Lys Tyr Gly Cys Trp Ser Gly Ser
115 120
Ala Thr Ile Met Pro Asp Gly Thr Pro Val Ile Met Tyr Thr Gly Val
130 135 140
Ser Arg Pro Asp Val Asn Tyr Glu Val Gln Asn Val Ala Phe Pro Lys
145 150 155 160
Asn Ser Ser Asp Pro Leu Leu Arg Glu Trp Val Lys Pro Ala His Asn
165 170 175
Pro Val Ile Val Pro Glu Gly Gly Ile Asn Ala Thr Gln Phe Arg Asp
180 185 190
Pro Thr Thr Ala Trp Tyr Ala Asp Gly His Trp Arg Ile Leu Val Gly
195 200 205
Ala Leu Ser Gly Ala Ser Arg Gly Val Ala Tyr Val Tyr Arg Ser Arg
210 215 220
Asp Phe Arg Arg Trp Thr Arg Val Arg Lys Pro Leu His Ser Ala Pro
225 230 235 240
Thr Gly Met Trp Glu Cys Pro Asp Phe Tyr Pro Val Thr Val Asp Gly
245 250 255
Lys Glu Ser Gly Val Asp Thr Ser Val Val Ser Ser Ser Arg Val Lys
260 265 270
His Val Leu Lys Asn Ser Leu Asp Leu Arg Arg Tyr Asp Tyr Tyr Thr
275 280 285
Val Gly Thr Tyr Asp Arg Leu Lys Glu Arg Tyr Val Pro Asp Asn Pro
290 295 300
Ala Gly Asp Lys His His Leu Arg Tyr Asp Tyr Gly Asn Phe Tyr Ala
305 310 315 320
Ser Lys Thr Phe Tyr Asp Pro Ser Lys Arg Arg Arg Ile Leu Trp Gly
325 330 335
Trp Ala Asn Glu Ser Asp Thr Ala Val Asp Asp Val Ala Lys Gly Trp
340 345 350
Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
355 360 365
Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Glu Ala Leu Arg Gly
370 375 380
Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
385 390 395 400
Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
405 410 415
Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
420 425 430
Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
435 440 445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
450 455 460
Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
465 470 475 480
Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
485 490 495
Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
500 505 510
Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
515 520 525
Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
530 535 540
Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
545 550 555 560
Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
565 570 575
Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
580 585

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<210> 176

<211> 670

<212> PRT

<213> Lolium perenne

<400> 176

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Met Pro Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala
 1          5          10          15
Ala Leu Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg
 20          25          30
Thr Gly Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu
 35          40          45
Leu Ala Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro
 50          55          60
Ala Gly Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val
 65          70          75          80
Ser Gly Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly
 85          90          95
Ala Ala Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn
100          105          110
Ala Phe Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe
115          120          125
His Phe Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val
130          135          140
Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly
145          150          155          160
Ala Ile Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp
165          170          175
Met Leu Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp
180          185          190
Tyr Asp Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp
195          200          205
Gly Arg Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln
210          215          220
Val Gln Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr
225          230          235          240
Asn Trp Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His
245          250          255
Val Gly Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly
260          265          270
Ser Asp Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg
275          280          285
Ala Gly Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu
290          295          300
Leu Val Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu
305          310          315          320
Cys Ile Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr
325          330          335
Glu Ala Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His
340          345          350
Val Met Lys Glu Ser Ser Asp Asp Arg His Asp Tyr Tyr Ala Leu
355          360          365
Gly Arg Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp
370          375          380
Ala Asp Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala
385          390          395          400
Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly
405          410          415
Trp Val Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp
420          425          430
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr
435          440          445
Gly Ser Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg
450          455          460
Thr Asn Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val
465          470          475          480
Phe Pro Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser
485          490          495
Phe Arg Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val
500          505          510
Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu

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<210> 177
<211> 514
<212> PRT
<213> Lolium perenne
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<400>	177															
Met	His	Ala	Asp	Pro	Asn	Gly	Pro	Val	Tyr	Tyr	Arg	Gly	Trp	Tyr	His	
1				5					10					15		
Leu	Phe	Tyr	Gln	Tyr	Asn	Pro	Glu	Gly	Ala	Val	Trp	Gly	Asn	Ile	Ala	
			20					25					30			
Trp	Gly	His	Ala	Val	Ser	Arg	Asp	Leu	Val	His	Trp	Arg	His	Leu	Pro	
		35					40					45				
Leu	Ala	Met	Val	Pro	Asp	Gln	Trp	Tyr	Asp	Ile	Asn	Gly	Val	Trp	Thr	
	50					55					60					
Gly	Ser	Ala	Thr	Val	Phe	Pro	Asp	Gly	Thr	Leu	Asn	Met	Leu	Tyr	Thr	
65					70				75						80	
Gly	Ser	Thr	Asn	Ala	Ser	Val	Gln	Ala	Gln	Cys	Leu	Ala	Val	Pro	Glu	
			85						90					95		
Asp	Pro	Asn	Asp	Ser	Leu	Leu	Arg	Asn	Trp	Thr	Lys	His	Glu	Ala	Asn	
			100					105					110			
Pro	Val	Leu	Leu	Pro	Pro	Pro	Gly	Ile	Gly	Asp	Lys	Asp	Phe	Arg	Asp	
		115					120					125				
Pro	Thr	Thr	Ala	Trp	Phe	Asp	Glu	Ser	Asp	Gln	Thr	Trp	Arg	Thr	Val	
	130					135					140					
Ile	Gly	Ser	Lys	Asp	Asn	Asn	Gly	His	Ala	Gly	Ile	Ala	Met	Val	Tyr	
145					150					155					160	
Lys	Thr	Lys	Asp	Phe	Leu	Asn	Tyr	Glu	Leu	Ile	Pro	Gly	Tyr	Leu	His	
				165					170					175		
Arg	Val	Asp	Gly	Thr	Gly	Met	Trp	Glu	Cys	Ile	Asp	Phe	Tyr	Pro	Val	
			180					185					190			
Gly	Gly	Lys	Asn	Gly	Ser	Glu	Glu	Leu	Tyr	Val	Ile	Lys	Glu	Ser	Ser	
		195					200					205				
Asp	Asp	Asp	Arg	His	Asp	Trp	Tyr	Thr	Leu	Gly	Lys	Tyr	Asp	Ala	Ala	
		210				215					220					
Ala	Asn	Thr	Phe	Thr	Ala	Ala	Asp	Pro	Glu	Asn	Asp	Leu	Gly	Ile	Gly	
225					230					235					240	
Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Phe	Tyr	Ala	Ser	Lys	Thr	Phe	Tyr	Asp	
				245					250					255		
Pro	Ala	Lys	Lys	Arg	Arg	Val	Leu	Trp	Gly	Trp	Ile	Gly	Glu	Thr	Asp	
			260					265					270			
Ser	Glu	Arg	Ala	Asp	Val	Ala	Lys	Gly	Trp	Ala	Ser	Leu	Met	Ser	Ile	
		275					280					285				
Pro	Arg	Thr	Val	Glu	Leu	Asp	Glu	Lys	Thr	Trp	Thr	Asn	Leu	Ile	Gln	
		290				295					300					
Trp	Pro	Val	Glu	Glu	Ile	Glu	Thr	Leu	Arg	Ile	Lys	Ser	Thr	Asp	Leu	
				310						315					320	

Gly Gly Ile Thr Ile Asp His Gly Ser Val Tyr Pro Leu Pro Leu His
 325 330 335
 Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg Leu Asp Ala Ala
 340 345 350
 Thr Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr
 355 360 365
 Ser Gly Gly Ser Thr His Arg Gly Ala Leu Gly Pro Phe Gly Ile Leu
 370 375 380
 Val Leu Ala Asp Gly Lys Ala Glu Gln Thr Ala Val Tyr Phe Tyr Val
 385 390 395 400
 Ser Lys Gly Leu Asp Gly Ala Leu Glu Thr His Phe Cys His Asp Glu
 405 410 415
 Ser Arg Ser Thr Leu Ala Lys Asp Val Val Lys Arg Val Val Gly Tyr
 420 425 430
 Thr Val Pro Val Leu Asp Gly Glu Ala Phe Ser Val Arg Val Leu Val
 435 440 445
 Asp His Ser Ile Val Glu Ser Phe Ala Met Gly Gly Arg Ser Thr Ala
 450 455 460
 Thr Ser Arg Val Tyr Pro Thr Glu Ser Ile Tyr Gly Ala Ala Gly Ala
 465 470 475 480
 Tyr Leu Phe Asn Asn Ala Thr Gly Gly Ser Val Thr Val Glu Lys Leu
 485 490 495
 Val Val His Glu Met Asp Ser Ser Tyr Asn Gln Ile Phe Met Ala Asp
 500 505 510
 Asp Leu

<210> 178

<211> 557

<212> PRT

<213> Lolium perenne

<400> 178

Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
 50 55 60
 Val Asp Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140
 Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155 160
 Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235 240
 Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly

										260						265						270		
Ala	Leu	Val	Asp	Leu	Val	Arg	Ala	His	Arg	Ile	Thr	Ile	Ala	Pro	Phe									
										275			280			285								
Val	Pro	Pro	Ile	Val	Val	Glu	Ile	Ala	Lys	Ser	Asp	Arg	Val	Gly	Ala									
										290			295			300								
Asp	Asp	Leu	Ala	Ser	Ile	Arg	Met	Val	Leu	Ser	Gly	Ala	Ala	Pro	Met									
										305			310			315			320					
Gly	Lys	Asp	Leu	Gln	Asp	Ala	Phe	Met	Ala	Lys	Ile	Pro	Asn	Ala	Val									
										325			330			335								
Leu	Gly	Gln	Gly	Tyr	Gly	Met	Thr	Glu	Ala	Gly	Pro	Val	Leu	Ala	Met									
										340			345			350								
Cys	Leu	Ala	Phe	Ala	Lys	Glu	Pro	Phe	Lys	Val	Lys	Ser	Gly	Ser	Cys									
										355			360			365								
Gly	Thr	Val	Val	Arg	Asn	Ala	Glu	Leu	Lys	Val	Val	Asp	Pro	Asp	Thr									
										370			375			380								
Gly	Ala	Ser	Leu	Gly	Arg	Asn	Gln	Pro	Gly	Glu	Ile	Cys	Val	Arg	Gly									
										385			390			395			400					
Lys	Gln	Ile	Met	Ile	Gly	Tyr	Leu	Asn	Asp	Pro	Glu	Ser	Thr	Lys	Asn									
										405			410			415								
Thr	Ile	Asp	Lys	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Leu	Val									
										420			425			430								
Asp	Asp	Asp	Asp	Glu	Ile	Phe	Ile	Val	Asp	Arg	Leu	Lys	Glu	Ile	Ile									
										435			440			445								
Lys	Tyr	Lys	Gly	Phe	Gln	Val	Ala	Pro	Ala	Glu	Leu	Glu	Ala	Leu	Leu									
										450			455			460								
Leu	Thr	Asn	Pro	Glu	Val	Lys	Asp	Ala	Ala	Val	Val	Gly	Val	Lys	Asp									
										465			470			475			480					
Asp	Leu	Cys	Gly	Glu	Val	Pro	Val	Ala	Phe	Ile	Lys	Arg	Ile	Glu	Gly									
										485			490			495								
Ser	Glu	Ile	Thr	Glu	Asn	Glu	Ile	Lys	Gln	Phe	Val	Ser	Lys	Glu	Val									
										500			505			510								
Val	Phe	Tyr	Lys	Arg	Ile	Asn	Lys	Val	Tyr	Phe	Thr	Asp	Ser	Ile	Pro									
										515			520			525								
Lys	Asn	Pro	Ser	Gly	Lys	Ile	Leu	Arg	Lys	Asp	Leu	Arg	Ala	Arg	Leu									
										530			535			540								
Ala	Ala	Gly	Ile	Pro	Thr	Glu	Val	Ala	Ala	Pro	Arg	Ser												
										545			550			555								

<210> 179

<211> 501

<212> PRT

<213> Lolium perenne

<400> 179

Met	Glu	Val	Leu	Leu	Leu	Glu	Lys	Ala	Leu	Leu	Gly	Leu	Phe	Ala	Ala						
										1			5			10			15		
Ala	Val	Leu	Ala	Ile	Ala	Val	Ala	Lys	Leu	Ala	Gly	Lys	Arg	Phe	Arg						
										20			25			30					
Leu	Pro	Pro	Gly	Pro	Ser	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln						
										35			40			45					
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Gly	Ile	Ala	Lys	Arg						
										50			55			60					
Phe	Gly	Glu	Val	Phe	Leu	Leu	Arg	Met	Gly	Ile	Arg	Asn	Leu	Val	Val						
										65			70			75			80		
Val	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val						
										85			90			95					
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly						
										100			105			110					
Asn	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys						
										115			120			125					
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala						
										130			135			140					
Gln	Asn	Arg	Val	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp						
										145			150			155			160		
Val	Lys	Ala	Asp	Pro	Ala	Ser	Ala	Thr	Ala	Gly	Thr	Val	Ile	Arg	Arg						
										165			170			175					

Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
 225 230 235 240
 Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
 325 330 335
 Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
 340 345 350
 Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
 355 360 365
 Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
 370 375 380
 Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
 385 390 395 400
 Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
 420 425 430
 Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Val Leu
 435 440 445
 Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
 450 455 460
 Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
 465 470 475 480
 Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
 485 490 495
 Lys Pro Leu Glu Ala
 500

<210> 180

<211> 361

<212> PRT

<213> Lolium perenne

<400> 180

Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45
 His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
 50 55 60
 Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
 65 70 75 80
 Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
 85 90 95
 Ile Val Gly Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
 100 105 110
 Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
 115 120 125
 Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln

130	135	140
Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala		
145	150	155
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe		160
	165	170
Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly		175
	180	185
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val		190
	195	200
Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp		205
	210	215
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala		220
225	230	235
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys		240
	245	250
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu		255
	260	265
Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met		270
	275	280
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile		285
	290	295
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr		300
305	310	315
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu		320
	325	330
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala		335
	340	345
Gly Ser Asn Ile Asp Asp Thr Ala Ala		350
	355	360

<210> 181

<211> 363

<212> PRT

<213> Lolium perenne

<400> 181

Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala		
1	5	10
Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala		15
	20	25
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly		30
	35	40
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala		45
	50	55
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys		60
65	70	75
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys		80
	85	90
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln		95
	100	105
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala		110
	115	120
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly		125
	130	135
Ala Val Thr Met Asp Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu		140
145	150	155
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr		160
	165	170
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg		175
	180	185
Gln Arg Gly Val Asp Leu Val Val Asn Pro Val Leu Val Ile Gly		190
	195	200
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys		205
	210	215
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr		220
225	230	235
		240

Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
 245 250 255
 Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
 260 265 270
 Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
 275 280 285
 Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
 290 295 300
 Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
 305 310 315 320
 Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
 325 330 335
 Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
 340 345 350
 Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
 355 360

<210> 182

<211> 360

<212> PRT

<213> Festuca arundinacea

<400> 182

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Glu Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
 210 215 220
 Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320
 Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
 325 330 335

Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
 340 345 350
 Ala Trp Ala Ile Glu Phe Thr Lys
 355 360

<210> 183
 <211> 543
 <212> PRT
 <213> Lolium perenne

<400> 183
 Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Ile Gln Asp Pro Leu
 1 5 10 15
 Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
 20 25 30
 Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
 35 40 45
 Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
 50 55 60
 Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
 65 70 75 80
 Lys Leu His Thr Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
 85 90 95
 Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
 130 135 140
 Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
 145 150 155 160
 Ala Leu Val Arg Ala Val Ala Arg Arg Thr Gly Glu Ser Val Asp Leu
 165 170 175
 Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
 180 185 190
 Phe Gly Ala Gly Ala Val Ala Ala Asp Ala Glu Glu Gly Asp Gly Ala
 195 200 205
 Gly Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu
 210 215 220
 Phe Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala
 225 230 235 240
 Asp Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Asn Ala Leu
 245 250 255
 Asp Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys
 260 265 270
 Asn Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe
 275 280 285
 Leu Pro Glu Ala Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp
 290 295 300
 Asp Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile
 305 310 315 320
 Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile
 325 330 335
 Glu Trp Ala Met Ala Glu Met Met His Ser Pro Asp Asp Leu Arg Arg
 340 345 350
 Leu Gln Gln Glu Leu Val Asp Val Val Gly Leu Asp Arg Asn Val Asp
 355 360 365
 Glu Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu
 370 375 380
 Thr Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala
 385 390 395 400
 Glu Asp Cys Val Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val
 405 410 415
 Met Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Arg Ala Trp Lys Asp
 420 425 430
 Ala Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala

		435					440				445				
Ala	Gly	Leu	Asp	Phe	Lys	Gly	Gly	Cys	Phe	Glu	Phe	Leu	Pro	Phe	Gly
	450					455					460				
Ser	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Met	Ala	Leu	Gly	Leu	Tyr	Ala	Leu
465					470					475					480
Glu	Leu	Ala	Val	Ala	Gln	Leu	Ala	His	Gly	Phe	Ser	Trp	Glu	Leu	Pro
				485					490					495	
Asp	Gly	Met	Lys	Pro	Ser	Glu	Leu	Asp	Met	Ser	Asp	Val	Phe	Gly	Leu
			500					505					510		
Thr	Ala	Pro	Arg	Ala	Thr	Arg	Leu	Phe	Ala	Val	Pro	Thr	Pro	Arg	Leu
		515					520					525			
Ala	Cys	Thr	Gln	Leu	Leu	Gly	Ala	Asp	Asp	Ala	Gly	Arg	Gln	Ala	
	530					535					540				

```
<210> 184
<211> 713
<212> PRT
<213> Festuca arundinacea
```

<400>	184														
Met	Glu	Cys	Glu	Asn	Gly	His	Val	Ala	Ala	Asn	Gly	Asp	Gly	Leu	Cys
1				5					10					15	
Val	Ala	Gln	Pro	Ala	Arg	Ala	Asp	Pro	Leu	Asn	Trp	Gly	Lys	Ala	Ala
			20					25					30		
Glu	Glu	Leu	Ser	Gly	Ser	His	Leu	Asp	Ala	Val	Lys	Arg	Met	Val	Glu
		35					40				45				
Glu	Tyr	Arg	Arg	Pro	Val	Val	Thr	Met	Glu	Gly	Ala	Ser	Leu	Thr	Ile
	50					55					60				
Ala	Met	Val	Ala	Ala	Val	Ala	Ala	Gly	Ala	Asp	Thr	Arg	Val	Glu	Leu
65					70					75					80
Asp	Glu	Ser	Ala	Arg	Gly	Arg	Val	Lys	Glu	Ser	Ser	Asp	Trp	Val	Met
			85						90					95	
Asn	Ser	Met	Ala	Asn	Gly	Thr	Asp	Ser	Tyr	Gly	Val	Thr	Thr	Gly	Phe
			100					105					110		
Gly	Ala	Thr	Ser	His	Arg	Arg	Thr	Lys	Glu	Gly	Gly	Ala	Leu	Gln	Arg
		115					120					125			
Glu	Leu	Ile	Arg	Phe	Leu	Asn	Ala	Gly	Ala	Phe	Gly	Thr	Gly	Ser	Asp
	130					135					140				
Gly	His	Val	Leu	Pro	Ala	Ala	Thr	Thr	Arg	Ala	Ala	Met	Leu	Val	Arg
145					150					155					160
Val	Asn	Thr	Leu	Leu	Gln	Gly	Tyr	Ser	Gly	Ile	Arg	Phe	Glu	Ile	Leu
				165					170					175	
Glu	Thr	Ile	Ala	Thr	Leu	Leu	Asn	Ala	Asn	Val	Thr	Pro	Cys	Leu	Pro
			180					185					190		
Leu	Arg	Gly	Thr	Ile	Thr	Ala	Ser	Gly	Asp	Leu	Val	Pro	Leu	Ser	Tyr
		195					200					205			
Ile	Ala	Gly	Leu	Val	Thr	Gly	Arg	Pro	Asn	Ser	Val	Ala	Thr	Ala	Pro
	210					215					220				
Asp	Gly	Ser	Lys	Val	Asn	Ala	Ala	Glu	Ala	Phe	Lys	Ile	Ala	Gly	Ile
225					230					235					240
Gln	His	Gly	Phe	Phe	Glu	Leu	Gln	Pro	Lys	Glu	Gly	Leu	Ala	Met	Val
				245					250					255	
Asn	Gly	Thr	Ala	Val	Gly	Ser	Gly	Leu	Ala	Ser	Ile	Val	Leu	Phe	Glu
			260					265					270		
Ala	Asn	Ile	Leu	Gly	Ile	Leu	Ala	Glu	Val	Leu	Ser	Ala	Val	Phe	Cys
			275				280					285			
Glu	Val	Met	Asn	Gly	Lys	Pro	Glu	Tyr	Thr	Asp	His	Leu	Thr	His	Lys
	290					295					300				
Leu	Lys	His	His	Pro	Gly	Gln	Ile	Glu	Ala	Ala	Ala	Ile	Met	Glu	His
305					310					315					320
Ile	Leu	Glu	Gly	Ser	Ser	Tyr	Met	Met	Leu	Ala	Lys	Lys	Leu	Gly	Glu
				325					330					335	
Leu	Asp	Pro	Leu	Met	Lys	Pro	Lys	Gln	Asp	Arg	Tyr	Ala	Leu	Arg	Thr
			340												

```

Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
370          375          380
Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
385          390          395          400
Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
          405          410          415
Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
          420          425          430
Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
          435          440          445
Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
          450          455          460
Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
465          470          475          480
Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
          485          490          495
Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
          500          505          510
Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
          515          520          525
Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
530          535          540
Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
545          550          555          560
Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
          565          570          575
Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
          580          585          590
Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
          595          600          605
Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
610          615          620
Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
625          630          635          640
Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
          645          650          655
Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
          660          665          670
Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
          675          680          685
Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
690          695          700
Trp Asn Gly Glu Pro Leu Pro Ile Cys
705          710

```

<210> 185

<211> 324

<212> PRT

<213> Lolium perenne

<400> 185

```

Met Ala Pro Ala Thr Pro Lys Asp Ser Ser Ala Leu Pro Gly Leu Leu
1          5          10          15
Leu Leu Phe Ala Ala Ala Thr Ser Val Ala Val Ala Asn Ala Gln Leu
          20          25          30
Ser Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu Thr Ile
          35          40          45
Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly Ala
          50          55          60
Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp
65          70          75          80
Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys Gly
          85          90          95
Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp Lys
          100          105          110
Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys Ala

```

[illegible]

```
<210> 186
<211> 398
<212> PRT
<213> Lolium perenne
```

<400> 186															
Met	Ala	Ala	Thr	Met	Thr	Val	Glu	Glu	Val	Arg	Lys	Ala	Gln	Arg	Ala
1				5					10					15	
Glu	Gly	Pro	Ala	Thr	Val	Leu	Ala	Ile	Gly	Thr	Ala	Thr	Pro	Ala	Asn
			20					25					30		
Cys	Val	Tyr	Gln	Ala	Asp	Tyr	Pro	Asp	Tyr	Tyr	Phe	Lys	Ile	Thr	Lys
		35					40					45			
Ser	Asp	His	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Phe	Lys	Arg	Met	Cys	Asp
	50					55					60				
Lys	Ser	Gln	Ile	Arg	Lys	Arg	Tyr	Met	His	Leu	Thr	Glu	Glu	Ile	Leu
65				70						75					80
Glu	Glu	Asn	Pro	Asn	Met	Cys	Ala	Tyr	Met	Ala	Pro	Ser	Leu	Asp	Ala
				85					90					95	
Arg	Gln	Asp	Ile	Val	Val	Val	Glu	Val	Pro	Lys	Leu	Gly	Lys	Ala	Ala
			100					105					110		
Ala	Gln	Lys	Ala	Ile	Lys	Glu	Trp	Gly	Gln	Pro	Arg	Ser	Lys	Ile	Thr
		115					120					125			
His	Leu	Val	Phe	Cys	Thr	Thr	Ser	Gly	Val	Asp	Met	Pro	Gly	Ala	Asp
	130					135					140				
Tyr	Gln	Leu	Thr	Lys	Met	Leu	Gly	Leu	Arg	Pro	Ser	Val	Lys	Arg	Leu
145				150						155					160
Met	Met	Tyr	Gln	Gln	Gly	Cys	Phe	Ala	Gly	Gly	Thr	Val	Leu	Arg	Leu
				165					170					175	
Ala	Lys	Asp	Leu	Ala	Glu	Asn	Asn	Arg	Gly	Ala	Arg	Val	Leu	Val	Val
			180					185					190		
Cys	Ser	Glu	Ile	Thr	Ala	Val	Thr	Phe	Arg	Gly	Pro	His	Glu	Ser	His
		195					200					205			
Leu	Asp	Ser	Leu	Val	Gly	Gln	Ala	Leu	Phe	Gly	Asp	Gly	Ala	Ala	Ala
	210					215					220				
Val	Ile	Ile	Gly	Ala	Asp	Pro	Asp	Val	Ser	Val	Glu	Arg	Pro	Leu	Phe
225				230						235					240
Gln	Leu	Val	Ser	Ala	Ser	Gln	Thr	Ile	Leu	Pro	Asp	Ser	Glu	Gly	Ala
				245					250					255	

```

Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
      260      265      270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
      275      280      285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
      290      295      300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
305      310      315      320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
      325      330      335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
      340      345      350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
      355      360      365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
      370      375      380
Val Val Leu His Ser Met Pro Ile Ala Ala Asp Ala Thr Ala
385      390      395

```

<210> 187

<211> 370

<212> PRT

<213> Festuca arundinacea

<400> 187

```

Met Lys Gln Glu Val Lys Ser Glu Met Asn Gly Glu Thr Met Ser Gly
 1      5      10      15
Asn Lys Gly Pro Val Val Val Thr Gly Ala Ser Gly Phe Val Gly Ser
      20      25      30
Trp Leu Val Met Lys Leu Leu Gln Ala Gly Tyr Thr Val Arg Ala Thr
      35      40      45
Val Arg Asp Pro Gly Asn Val Glu Lys Thr Lys Pro Leu Leu Glu Leu
      50      55      60
Pro Gly Ala Lys Glu Arg Leu Ser Ile Trp Arg Ala Asp Leu Ser Glu
      65      70      75      80
Glu Gly Ser Phe Asp Glu Ala Ile Ala Gly Cys Thr Gly Val Phe His
      85      90      95
Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu Asn Glu Val
      100      105      110
Ile Lys Pro Thr Val Glu Gly Met Leu Ser Ile Met Arg Ala Cys Lys
      115      120      125
Glu Ala Gly Thr Val Lys Arg Val Val Phe Thr Ser Ser Ala Gly Thr
      130      135      140
Val Asn Ile Glu Glu Arg Pro Arg Pro Ala Tyr Asp Gln Asp Asn Trp
      145      150      155      160
Ser Asp Ile Asp Phe Cys Arg Arg Val Lys Met Thr Gly Gln Met Tyr
      165      170      175
Phe Val Ser Lys Ser Leu Ala Glu Lys Ala Ala Met Asp Tyr Ala Lys
      180      185      190
Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val Val Gly
      195      200      205
Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala Leu Ala
      210      215      220
Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln Val Gln
      225      230      235      240
Leu Val His Leu Asp Leu Cys Asp Ser Met Thr Tyr Leu Phe Glu
      245      250      255
His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp Thr Thr
      260      265      270
Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu Tyr Asp
      275      280      285
Ile Pro Gln Lys Phe Pro Gly Val Asp Asp Asp Leu Gln Pro Ile His
      290      295      300
Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg Tyr Thr
      305      310      315      320
Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu Lys Gly

```

```

          325          330          335
Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser Ala Ala
          340          345          350
Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile Gly Ala
          355          360          365
Glu Thr
          370

```

<210> 188
 <211> 329
 <212> PRT
 <213> Lolium perenne

```

<400> 188
Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
 1          5          10          15
Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
          20          25          30
Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
          35          40          45
His Leu Leu Ala Leu Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
          50          55          60
Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
          65          70          75          80
Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asp
          85          90          95
Leu Val Leu Asp Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
          100          105          110
Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
          115          120          125
Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
          130          135          140
Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
          145          150          155          160
Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
          165          170          175
Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
          180          185          190
Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
          195          200          205
Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
          210          215          220
Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
          225          230          235          240
Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
          245          250          255
Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
          260          265          270
Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
          275          280          285
Pro Gly Leu Val Arg Ala Glu Ala Val Pro Lys Lys Leu Met Ala Leu
          290          295          300
Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
          305          310          315          320
Ser Leu Lys Ser Arg Gly Cys Ile Ala
          325

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<210> 189
 <211> 330
 <212> PRT
 <213> Lolium perenne

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<400> 189
Met Val Ser Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly
 1          5          10          15
Phe Val Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His

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      20      25      30
Val Ile Gly Thr Val Arg Asp Pro Gly Asn Arg Arg Lys Val Gly His
      35      40      45
Leu Trp Lys Leu Pro Gly Ala Asn Glu Arg Leu Gln Leu Val Arg Ala
      50      55      60
Asp Leu Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Arg Ala Cys Glu
      65      70      75      80
Gly Val Phe His Ile Ala Ser Pro Val Leu Gly Lys Ser Asp Ser Asn
      85      90      95
Cys Lys Glu Ala Thr Leu Gly Pro Ala Ile Asn Gly Thr Leu Asn Val
      100      105      110
Leu Arg Ser Cys Lys Lys Ser Pro Phe Leu Lys Arg Val Val Leu Thr
      115      120      125
Ser Ser Ser Ser Ala Val Arg Ile Arg Asp Glu Thr Gln Gln Pro Glu
      130      135      140
Leu Leu Trp Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys
      145      150      155      160
Leu Gln Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala
      165      170      175
Leu Asp Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Thr Val Leu Pro
      180      185      190
Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Thr Thr Ala
      195      200      205
Ser Asp Ile Leu Gly Leu Leu Gln Gly Asp Thr Asp Arg Phe Thr Leu
      210      215      220
Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Ser His
      225      230      235      240
Ile Leu Val Tyr Glu Thr Pro Glu Ala Thr Gly Arg Tyr Leu Cys Ser
      245      250      255
Ser Val Val Leu Asp Asn Asn Glu Leu Val Gly Leu Leu Ala Lys Gln
      260      265      270
Phe Pro Val Phe Pro Ile Pro Arg Arg Leu Lys Asn Pro Tyr Gly Lys
      275      280      285
Gln Ala Tyr Gln Leu Asp Thr Ser Lys Leu Gln Gly Leu Gly Leu Lys
      290      295      300
Phe Lys Gly Val Gln Glu Met Phe Asn Asp Cys Val Glu Ser Leu Lys
      305      310      315      320
Asp Gln Gly His Leu Leu Glu Cys Pro Leu
      325      330

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<210> 190

<211> 326

<212> PRT

<213> Lolium perenne

<400> 190

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Met Ala Pro Ala Thr Pro Lys Asp Ser Ser Ser Ser Ala Leu Pro Gly
  1      5      10      15
Leu Leu Leu Leu Leu Ala Ala Ala Thr Ser Val Ala Val Ala Asn Ala
      20      25      30
Gln Leu Ser Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu
      35      40      45
Thr Ile Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met
      50      55      60
Gly Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly
      65      70      75      80
Cys Asp Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu
      85      90      95
Lys Gly Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile
      100      105      110
Asp Lys Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser
      115      120      125
Cys Ala Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu
      130      135      140
Gly Gly Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr
      145      150      155      160

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Ala Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn
 165 170 175
 Leu Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr
 180 185 190
 Asp Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys
 195 200 205
 Gln Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala
 210 215 220
 Phe Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly
 225 230 235 240
 Asn Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly
 245 250 255
 Tyr Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln
 260 265 270
 Ala Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala
 275 280 285
 Ser Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Met Val Lys
 290 295 300
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 305 310 315 320
 Asn Cys Arg Ala Val Asn
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26

<210> 192
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<220>
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<400> 192
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21

<210> 193
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 <212> DNA
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<220>
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28

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<210> 195
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<210> 202
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<213> Artificial Sequence

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<220>
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<210> 206
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20